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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on:

March 26, 2003, 04:18:30; Search time 4821.31 Seconds (without alignments) 15096.740 Million cell updates/sec

US-09-702-134-7212\_COPY\_28000\_30500 2501 .

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Sequence:

Perfect score:

Title:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database:

gb\_sts:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

AC096690 145999 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBa0059G06, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 ordered pieces. RESULT 1 AC096690/c LOCUS ACCESSION VERSION KEYWORDS SOURCE ORGANISM DEFINITION

AC096690.

AC096690.4 G1:20503077

HTGS\_PHASE2.

Oryza sativa.

I (bases 1 to 145999).

Buell.C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,

REFERENCE AUTHORS

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Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B., Jih, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J., Quockenbush, J., White, O., Salzberg, S. and Fraser, C. Gupulsished Oupublished Unpublished Unpublished Unpublished Uncert Submission Direct Submission Medical (22-SFP-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA 3 (bases I to 145999) Medical Center Dr, Rockville, MD 20850, USA	ulasion OB MAY-2002) The Ins ter Dr. Rockville, M 602 this sequence ve s is a 'working draf of 5 contings. Gaps bosented as runs of N. ed to be correct as ps between them are by the submittor. ence will be replace inished sequence as s sion number will be 3002: conting of 71267: conting of 71267: conting of	968 94679: contig of 23315 868 94779: gap of unknown 868 94779: gap of unknown 221 122320: gap of unknown 81 14599: contig of 23675 81 14599: contig of 23675 10. 14599  /organism="Oryza sativa" /organism="Oryza sativa" /db_xref="taxon:4530" /chromosome="3" /chromosome="3" /chomosome="0SJNB80059006" /clone="0SJNB80059006" /clone="0SJNB80059006	۲a م	AIGTCCAAGATAAANTIGGCCCAAGTGAAAAACTCAGAACTACATAAATATTTTCGCAA 60	AAAACCCATTTCACATATGGATCTGTGAGGAGGCTGCTTGCAAACTGATTTTGCAG 180  AAAACCCATTTCACATATGGATCTGTGAGGAGGCTGCTTGCAAACTGATTTTTGCAG 180  AAAACCCATTTCACATATGGATCTGTTGAGGAGCTGCTTGCAAACTGATTTTTGCAG 115357  GCAGGCAAGTAAGGACTTTCGACTAGAACGATTTTTTTTAAAAAAAGAATAAACC 240
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"., Yuan, Q. Ouyang, S., Liu, J., Tallon, L., Gansberger, K., Yerron II, L., Berra, J., Tsitrin, T., Krol, M., Jarrahi, S., Yoo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Yan, Tang, Q., Haas, S., Suh, B., Peterson, J., Sh, J., White, O., Salzberg, S. and Fraser, C. Mitcho., Salzberg, S. and Fraser, C. Liva ssp. japonica cv. Nipponbare OSJNBb0062019 BAC genomic
244803 bp DNA linear HTG 20-JUL-2002 lva chromosome 3 clone OSJNBb0062G19, *** SEQUENCING IN ***, 33 unordered pieces.
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Center Dr. Rockville, MD 20850, USA
This is a "working draft" sequence. It currently
ts of 33 contigs. The true order of the pieces
Known and their order in this sequence record is
ary. Gaps between the contigs are represented as
f N, but the exact sizes of the gaps are unknown.
econd will be updated with the finished sequence
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/chromosome="3"
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SOURCE  Organ sativa  Organ sativa  Organ sativa  Enkraptota; Viridiplantae; Streptophyta; Embryophyta; Itacheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enthartochodeae; Orgace; Orgace; Orgace; I chases 1 to 1598)  AUTHORS TOYOMASU, T., Kawaide, H., Sekimoto, H., von Numers, C., Phillips, A., Hedden, Y. and Kamiya, Y.  TITLE Cloning and characterization of a cDNA encoding gibberellin 20-oxidase from rice (Orgac sativa L.) seedlings  AUTHORS Kamiya, Y.  TITLE Direct Submission  JOURNAL Grantya, Y.  TITLE Direct Submission  JOURNAL Submitted (29-FEB-1996) Yuji Kamiya, Plant Hormone Function, Frontier Research Prooram, RIKEN, Hirosawa 2-1, Wake-shi, Saitame	351-01, Japan  FEATURES Location/Qualifiers 1. 1598 /organism="Cryza sativa" /db_xref="taxon:4530" 1701285 /codon_start=1 /product="qibberellin c-20 oxidase" /profice:="qibberellin c-20 oxidase" /db_xref="qibberellin c-20 oxidase" /db_xref="qibberellin c-20 oxidase" /db_xref="qibberellin c-20 oxidase" /db_xref="qi:1854637" /db_xref="qi:1854637"	EKORRSGARGETAVASSFEGRASKILPWKETLISFRYSSADEBEGEGGGELIVARIGAS FEGRASKILPWKETLISFRYSSADEBEGEGGGELIVARIGAS FEGRALOZEN SENGRESEN SE	vative (CCTGGGATGA GCTGGGATGA GCTGGGATGA GCTAGTTAAAAAAAAAA	696 ATCTCCATCGGTTAATTAATTGATTGATAGCTAGATTATCAACAATTAATGAGGGGGG 75	QY         BIA CUSTOGRAGATE CONTROLL           BIA CUSTOGRAGATE CONTROLL         BIA CUSTOGRAGATE CONTROLL           BIA CUSTOGRAGATE CALTANGE CONTROLL         BIA CUSTOGRAGATE CALTANGE CONTROLL           BIA CUSTOGRAGATE CALTANGE CONTROLL         BIA CUSTOGRAGATE CALTANGE CONTROLL           BIA CALTANGE CONTROLL         BIA CALTANGE CONTROLL           BIA CALTAGA CONTROLL	
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GEVYARYCSEMSRLSILEIMEVLGESLGVGRAHYRRFFEGNDSIMRINYTPPCGRPLET
LGTGPHCDPFISLITHQDNWGGLQVHFBCRRRSIRRRSDARVVNIGDFFMALSGRYRK
SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDASNPRAYDDFTWRSLIDFTQK
HYRANKTLEVFSSWIYQQQQGLALQPAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long Ashton Research Station, Dept. of Agricultural Sciences, University of Eristol, Long Ashton, Bristol. BS18 9AF UK 2 (bases 1 to 1451) Appleford, N.E.J. (cloning and characterisation of cDNAs encoding gibberellin 20-oxidase from wheat (Triticum aestivum L.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                  1451 bp mRNA linear PLN 25-JUN-1997 for gibberellin 20-oxidase, clone S37E.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta;—Magnollophyta; Lilliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 1451)
Appleford, N.E.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       836 GGCGGAGGAGAGCCCCGGGTCGGTGGCGGAGGAGCTGGAGGTGGCGCTGATCGACGT 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/db_xref="GI:2222800"
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1559 GICGACTATIGITGGICGTACGATATTATATTATATA 1597
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0; Mismatches 228
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/db_xref="taxon:4565"
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from wheat and

20-oxidase gene

Poaceae;

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2 (bases 1 to 1343)
Youssefian, S.
Direct Submission
Submitted (04-JUL-1997) Shohab Youssefian, Akita Prefectural
College of Agriculture, Biotechnology Institute; 2-2 Minami,
Obgatamura, Minamiakita-gun, Akita 010-04, Japan
(B-mail:shohab@air.akita-u.ac.jp, Tel:0185-45-2026,
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Pooideae; Triticeae; Triticum.
                                                  Characterization of a gibberellin
its expression in trangenic rice
                                       Youssefian, S.
                                                                            Unpublished
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Matches
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                                       AUTHORS
                         REFERENCE
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                                                                                        REFERENCE
                                                                                                      AUTHORS
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                                                                                                                                                                                              FEATURES
                                                   TITLE
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                                                                                                     GTCCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCATCGGCTGGAGATGAAGA 1180
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                                                                                                                    481 CTCCAAGCTGCCGTGGAAGGACCCTCTCCCTTCCGGTCCTGCCCGTC--
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/tissue\_type="leaf tissue" /clone\_lib="lamda gil0" /dev\_stage="6-week-old dwarf plants" 1. .1343

/organism="Triticum aestivum"

Location/Qualifiers

1. .1343

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/function "Gibberellin Biosynthesis

/codon\_start=1

/gene="wga20" /gene="wga20"

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SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDAANPRAIPDFTWRSLLDFTQR
HYRADMKTLEVFSSWIVQQQQQPQPART"
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                                                                                                                                                                                                                                                                                                                             DB 8;
                                                                                                                                                                                                                                                                                                                           Score 596.8; DB 8;
Pred. No. 8.3e-82;
0; Mismatches 252;
                                                                                                                                                                                                                  /gene="wga20"
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482 c 408 g 241 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGCTGGAGGTGGCGCTGATCGACGTGGGGGGCGGGG
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les 827; Conserv
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PLN 10-JUL-1997

mRNA linear complete cds.

1343 bp for wga20,

Triticum aestivum mRNA AB005555 AB005555.1 GI:2257602

AB005555

DEFINITION

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

Triticum aestivum (strain:Rht3 Dwarf, isolate:April Bearded) 6-week-old dwarf plants leaf tissue cDNA to mRNA, clone\_lib:lamda gtl0 clone:wga20. Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORGANISM

AUTHORS Appleford,N.E TITLE Cloning and c Cloning and c JOURNAL Unpublished FEATURES Loca source //org	/041 /045 /045 /15 /045 /040 /040	/evi /pro /pro /db_ /db_ /db_ /tra /cra	GEVY CATO CATO CATO SCIA HYRA BASE COUNT 263 a ORIGIN Ouery Match	Best Local Similarity Matches 827; Conserva Qy 749 CARGGEGEGEGEA Db 97 CTRGGEGEGEGEA	∞ ∺ ∞	Db 217 GGAGCTGCAGTCCC Qy 914 GTCGTCGGTGGTCCG Db 277 CGCCGAGGTGACGCG Qy 974 TAACCAGGCATCGA	Db 337 GAACCACGGTATCON QY 1034 CACGCTGCCGCTGGG QY 1094 CGCCAGCACCTCCC QY 1094 CGCCAGCAGCTTCAC QY 154 CGCCAGCAGCTTCAC QY 154 CGCCAGCAGCTTCAC QY 1554 CGCCAGCAGCTTCAC	517 1214 565 1274
OY 1094 CGCCAGCAGCAGCTTCACGGGGCGTTCAACCTGCCGTGGAAGGAA	QY         1214 GAAGCTCGGGGGGGCGCGGGGCGGGGGGGGGGGGGGGGG	QY         1334 AGACCGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAA 1393           Db         712GCCGCGCCCACTACTTCGAGGCAACGACTCCATCCATCGATGCGCCTCAA 766           QY         1394 CTACTACCGGGGTGCCACTCGACGCTGGGGACCGGTCCGCACTGCGACC           14 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         1454 CACCTGGCTCACCATCCTCCACGAGACCACGTGGGGGGGG			OY 1754 GCTGCTGGACTTCACGCAGCGCCCACACTGCACATGCGCACGCTTCTC 1813	TAX14007  TAX14007  LOCUS  TAX14007  TAX14000  TAX14000	Spermatophyta; Magnoliophyta; Illiopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum. AUTHORS Appleford, N.E. TITLE Direct Submission JOURNAL Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long Ashton Research Station, Dept. of Agricultural Sciences, University of Bristol, Long Ashton, Bristol. BS18 9AF UK C bases 1 to 1431)

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RADMKTLEVPSSRLAFTCQPPADGTLVDAANPRAYDDFTWRSLLDFTQK
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                                                                                                                                                                                                                                                                                                            "degrees C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 596.8; DB 8; Length 1431;
Pred. No. 8.3e-82;
0; Mismatches 252; Indels 39; Gaps
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characterisation of cDNAs encoding gibberellin rom wheat (Triticum aestivum L.)
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                                                                                                                                                                                                                                                issue_type="scutellum"
tone_lib="rambdaZapScut"
sv_stage="germinating grain 3 days at
). .1198
                                                                                                                                                                                                                                                                                                                                                                             vidence=experimental
roduct="gibberellin 20-oxidase"
rotein_id="CAA74330.1"
__xref="G1:222796"
                                                                                                                          ganism="Triticum" aestivum"
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                                                                                                                                                                    1ltivar="Maris Huntsman"
._xref="taxon:4565"
.one="$448"
                                                                         ation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           don_start=1
                                                                                                                                                  rain="Rht3
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/evidence=experimental
/protain_id="caA74331.1"
/brotain_id="caA74331.1"
/db_xref="SPTREMBL:004706"
/db_xref="SPTREMBL:004706"
/tb_xref="SPTREMBL:004706"
/translation="MYQPYEDAAPLSGRADIPSQFIWPEGESPTPDAARELHVPLIDIGML:SGPPRATELAPAHRCUDAFFTHPLPER
GGMLSGPPRATENTRIVELVERAGERGFFQVNHGIDAELLADAHRCUDAFFTHPLPER
QRALRRPGESCGYASSFTGRFASKLPWKETLSFRSCPSDPALVVDYIVATIGEDHRRL
                                                                                                                                                                                               GEVYARYCSEMSRLSLEIMEYLGESLGVGRAHYRRFFEGNDS IMRLNYYPPCORPMET
LGTGPHCDPT SLTILHQDNVGGLQVHTEGRWRSIRPRADAFVVNIGDTFMALSNGRYK
SCLHRAVVNSKVPRKSLAFFLCPEMDKVVAPPGTLVDAANPRAYPDFTWRSLLDFTQK
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                                                                                                                                                                                                                                                                                                                                             Score 590.6; DB 8; Length 1446; Pred. No. 7.4e-81; 0; Mismatches 239; Indels 39;
                                                                                                                                                                                                                                                             HYRADMKTLEVFSSWIVQQQQQQLLPPLASH"
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           /codon_start=1
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74.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATIA1008 1446 bp mRNA linear PLN 25-JUN-1997
Triticum aestivum mRNA for gibberellin 20-oxidase, clone S39A.
Y14008
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Triticum aestivum.
Triticum aestivum.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticae; Triticum.
Appleford,N.E.
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                                              1334 AGACCGCCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAA 1393
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        677
                                                                                                                                                                                                                                       793 GACGTCCCTGACCATCCTCCACCAGGACAACGTCGGCGGCCTGCAGGTGCACGAGGG
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/clone_lib="LambdaZapScut"
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/db_xref="taxon:4565"
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GEATARYCSEMSKLSLEHWYLGESLGVRGAHR RRFFEGREIMELMELYPPCQXPNET
LGYGPHODPTSLITTHQDDVGGLQVHADGRWLSIRRRADAFVVNIGDTFWALSNGRYR
SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPETLVDEANPRAYPDFTWRALLDFTQK
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20-oxidase mRNA, complete cds.
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GGLLSGDRAAAAEVTRLVGDACERHGFPQVVNHGIDAELLADAHRCVDAFFTMSLQGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pooldeae; Poeae; Lollum.

1 (bases 1 to 1111)

Xu,J., Lange,T. and Altpeter,F.

Cloning and characterization of a cDNA encoding a multifunctional gibberellin 20-oxidase from perennial ryegrass (Lolium perenne L.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
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997 GTACAAGAGTIGTCTCCACCGCGCTGTCGTGAACAGCAAGGTCCCGAGGAAGTCGCTGGC
                                                                                              CITCITCCTCTCCCCGGAGATGGACACGGTGGGTGCGCCCGCCGGAGGAGCTGGTCGACGA
                                                                                                                                                    CCACCACCGAGGGTGTACCCGGACTTCACGTGGCGGGCGCTGCTGGACTTCACGCAGCG
                                                                                                                                                                                                       1775 CCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGGACTGGCTTAATCATCATCG
                                         39;
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Pred. No. 3.3e-80;
0; Mismatches 231;
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/product="gibber=11in 20-oxidase"
/protein_id="AA643044 1"
/db_xref="GI:13625523"
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/cultivar="Limes"
/db_xref="taxon:4522"
                                                                                                                                                                                                                                                                                                                                                    Lolium perenne clone 1 gibberellin AX014280
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                                                                                                                                         186 CGCCGACGCCTGCCGCCACGCCTTCCTACCAGGTCGTCAACCACGGCATCGACGCCGA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Xu, 2. Lange,T. and Altpeter,F.
Direct Submission
Submitted (24-NOV-2000) AG Gentransfer, Department of Molecular
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                                                                                                                                                                                            GCGGCGCCTGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGGA 1294
                                                                                                                                                                                                                                                                       GCTGATGGAGGTGCTCGGGGAGGCCTGGGCATCGTCGGAGACCGGCGCCCACTACTTCCG 1354
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                                                                           GTTCGCGTCCAAGCTACCGTGGAAAAAGCTTGTCGTTCCGTTCCTGTCCGTC---
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//translation="MVQPYPDAALLSGQSDIPSQFIWPADESPSEDATEELHVPLIDI
GGLLSGDREAABVTRLVGDACERHGEFQVVNHGIDAELLADAHKCVDAFFWALDDE
GGLLSGDREAABVTRLVGDACERHGEFGVVNHGIDAELLADAHKCVDAFFWALDGD
RALARPGESCGYASSFTGRFASKLPRKEPESRSCPSEDLVVDYTVATLGEDHRRL
GEVYARYCSEMSRLSLEIMEVLGESLGVGRAHYRRFFEGNESIMRLNYYPPCQRPNGT
IGTGPHCDPTSLTITHQDDVGGLQVHADGRVLSIRPRADARVNHGDTFWALLSNGRYK
SCLHRAVNISRVPRKSLAFFLCPEMDKVVAPPGTSVDEANPRAYPDFTWRALLDFTQK
HYRADMKTLEWFSDRVALDFTTTTTTQDQRTYTRASASLHLLACCT"
418 c 368 9 196 t
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                                                      15-APR-2001
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                                                                                                                                                                                          Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-NOV-2000) AG Gentransfer, Department of Molecular Cell Biology, Institute of Plant Genetics and Crop Plant Research, Correnstr. 3, Gatersleben D06466, Germany Location/Qualifiers
                                                                           complete cds.
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                                                                                                                                                                                          Embryophyta; Trach
a; Poales; Poaceae;
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                                  Lolium perenne clone 4 gibberellin 20-oxidase mRNA, AY014276
AX014276.1 GI:13625518
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/protein_id="AAG43042.1"
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Pred. No. 5.5e-79;
0; Mismatches 236;
                                                                                                                                                                                          Streptophyta; Em
/ta; Liliopsida;
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/cultivar="Limes"
/db_xref="taxon:4522"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="GA 20-oxidase"
                                                                                                                                                                                                            Spermatophyta; Magnoliophyta;
                                                                                                                                                                      Lolium perenne
Eukaryota; Viridiplantae;
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1 (bases 1 to 1175)
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Best Local Similarity 74.4%;
Matches 799; Conservative
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                                                                                                                                                   Lolium perenne
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                                                                                                                                                                        /product="gibberellin 20-oxidase"
/protein_id="AaG43045.1"
/db_xref="G1:1862555"
/tanslation="WQ2VFDAALLSAQSDIPSQFIWPADESPTPDATEELHVPLIDI
GGLLSGDRRAAABTWRLVGDAOERHGFFQVVNHGIDAELLGHARCYDAFFTMSLQDKQ
RALRRPGESCGFASSFIGRFASKLPWKETLSFRSCPSEPDLVVDYIVATLGEDHRRLG
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CLHRAVVNSRYPRKSLAFFLCPEMDKVVAPPGTLVDEANPRAYDFTWRALLDFTQKH
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Cell Biology, Institute of Plant Genetics and Crop Plant Research, Correnstr. 3, Gatersleben D06466, Germany
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Pred. No. 1.6e-77
0; Mismatches 23
                                                                                                                                                                                                                                                                                                                    YRADMKTLEVFSDWIQQGHQPAATTTTT"
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                                                             /organism="Lolium perenne"
/cultivar="Limes"
/db_xref="taxon:4522"
                                                                                                                                           /note="GA 20-oxidase"
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                                 Location/Qualifiers
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Best Local Similarity 74.5%;
Matches 800; Conservative
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SCLHRAVVNSRVPRKSLAFFLCPEMDKVVAPPGTLVDBANPRAYPDFTWRALLDFTQK
HYRADMKTLEVFSDWIQQGHQPAATTTT"

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GEVYARYCSEMSRLSLEIMEVLGESLGVGRAHYRRFFEGNESIMRLNYYPPCQRPNET
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Xu,J., Lange,T. and Altpeter,F.
Direct Submission
Submitted (25-NOV-2000) AG Gentransfer, Department of Molecular
Cell Biology, Institute of Plant Genetics and Crop Plant Research,
IPK-Gatersleben, Correnstr. 3, Gatersleben D06466, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lolium perenne.
Lolium perenne.
Lolium perenne
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Pooldeae; Poeae; Lolium.
1 (bases 1 to 2128)
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Cloning and characterization of a cDNA encoding a multifunctional
gibberellin 20-oxidase from perennial ryegrass (Lolium perenne L.)
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GCCCAACGAAACCTGGGCACGGCCCGCACTGCGACCGGACGTCGCTCACCATCCTCCA
                                                                                                                                                                                                                                                      939 GGCCAACCGCGGGCGTACCGGACTTCACGTGGCGGGCGCTGCTGGACTTCACGCAGAA
                                                                                          819 CTACAAGAGCTGCCTCCACCGCGCCGTCTCAACAGCCGTGTGCCCAGGAAGTCGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1775 CCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAATCA 1828
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LOLium perenne gibberellin 20-oxidase gene, complete cds. AVO14277
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/product="glabberellin 20-oxidase"
join(860. .1341,1436. .2045)
/note="GA 20-oxidase"
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/protein_id="AAG43043.1"
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/db_xref="taxon:4522"
661. .666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .2128
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CGGAGGAGCTGGTCGACGACCACCACCAGGGTGTACCCGGACTTCACGTGGCGGCGC 1755
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Location/Qualifiers
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1. .1170
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                                                                                                                                                                                                                                                                                                                                                                                 GI:20152206
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Best Local Similarity 63.77
Matches 676; Conservative
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AB077025
LOCUS
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JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1336 ACCGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1396 ACTACCCGGCGTGCCAGAGGCCACTCGACACGGTGCGGTCCGCACTGCGACCCCA 1455
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                                                                                                                                                                                                                                                                                                                                                          1165 GCAGGGCGCGCCCCGGCGCACGACGACCACCAGCAACACATCACCGGCCG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1115 CTTCGCGTCCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCATCGGCTGGAGA 1174
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                                                                                                                                                                                                                                                                                                  985 CGACATCGGGGGCCTCCTCTCCGGCGACCGCGTCGCGGCCGCCGAGGTGACGCGCCTTCGT 1044
                                                                                                770 GGAGGIGGIGITCGACGCGGCGGIGCIGAGCGGGCAGACGGAGAICCCGICGCAGITCAT 829
                                                                                                                       830 ATGGCCGCCGCGCAGCAGAGCCCCCGGGTCGGTGGAGGAGCTGGAGGTGGCGCTGAT 889
                                                                                                                                                                                                                                                          935 GGGGGAGGCGIGCGAGGCCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGCC 994
                                                                                                                                                                                                    925 CTGGCCGGGGGGGGGCCCGTCCCCGGACGCACCGAGGAGCTGCACGCCTCAT
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                                                          Indels 103;
                  Length 2128;
              Score 499.4; DB 8;
Pred. No. 6.7e-67;
0; Mismatches 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1175 TGAAGAGGCGAGGAGGCGTGGGTGAGTACCTGGT-----
                20.0%;
68.4%;
                                                        Matches 789; Conservative
                                       Similarity
                  Query Match
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Oryza sativa (japonica cultivar-group) mRNA for GA C20oxidase2, AB077025
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PFWWPNGDARPASAAELDMPVVDVGVLRDGDAEGLRRAAAQVAAACATHGFFQVSEHG
VDAALARAALDGASDFFRLPLAEKRRARRVPGTVSGYTSAHADRFASKLPWKETLSFG
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REFFADSSSIMRCNYYPPCPBPERTLGTGPHCDPTALTILLQDDVGGLEVLVDGEWRP
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SAATPQHYPDFTWADIMRFTQRHYRADTRTLDAFTRWLAPPAADAAATAQVEAAS"
455 c 392 g 152 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sasaki, A., Ashikari, M., Ueguchi-Tanaka, M., Itoh, H., Nishimura, A., Swapan, D., Ishiyama, K., Saito, T., Kobayashi, M., Khush, G.S.,
1936 TGCTGGACTTCACGCAGAAGCACTACCGGGCCGACATGAAGACGCTCGAGGTGTTCTCCG 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1170)
Maksuoka,M., Sasaki,A. and Ashikari,M.
Direct Submission
Submitted (25-DEC-2001) Makoto Matsuoka, Nagoya University,
BioScicence Center; Furocho, Chikusa, Nagoya, Aichi 464-8601,
(F-māli:makoto@nugail.agr.nagoya-u.ac.jp, Tel:81-52-789-5225,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green revolution: A mutant gibberellin-synthesis gene in rice
Nature 416 (6882), 701-702 (2002)
21959433
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
                                                                                                 TECTGGACTICACGCAGCGCCACTACAGGGCCGACATGCGCCACGCTTCAGGCCTTCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; iilliopsida; Poales; Poaceae;
Bhrharroideae; Oryzae; Oryza.
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Pred. No. 1e-46;
); Mismatches 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="GA C200xidase2"
/protein_id="BAB89356.1"
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APAAAVCDLRMEPKIPE
YAAACATURPERFQVSEHG
AADREASKLPWKETLSFG
GTINELLELSLGVERGYY
CODDVGGLEBVLYDGEWRP
SLAFFLCPREDRVVRPPP
PAADAAATAQVEAAS"
PLN 26-JUN-2002
-oxidase mRNA,
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                                                                                        1; Tracheophyta;
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GCTCTGGC 323
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GTGGCCGC 263
                                                                                                                                              a defective
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GTCGACGT 203
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FTCGTGTG 143
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                                                                                                                                                                    2002)
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REFERENCE 2 (bases 1 to 1513)  AUTHORS Garda-Marthnez, L., Lopez-Diaz, I., Sanchez-Beltran, M.J., Phillips, A.L., Ward, D.A., Gaskin, P. and Hedden, P.  TITLE Direct Submission JOURNAL Submitted (12-SEP-1996) Instituto de Biologia Molecular y Celualz de Plantas, Universidad Politecnica/CSIC, Camino de Vera s/n, Valencia 4602, Spain FEATURES 1. 1513 Source 1. 1513 Action/Qualifiers 1. 1513 Action="Paylor Horticultural" Action Actio	/ db_xref="G1:2108432" //translation="MalDMHPIPIMPOPSWQEIKBQDQHPI //translation="MalDMHPIPIMPOPSWQEIKBQDQHPI //WPDEERACINPEELPYPFIDLGGFLGGDPLAATERSRLYG QQLISDAHLYMDHFFALPLSHKQRAQRWPGEHCGYASSFTG PRINDSQLTYVBVICLORAGNERFERFGNYVDYCEAMSNLSLC EFFEENNSIMMLYYPPCQKPDITLGTGPHODPTSLTILLIG KPDVNAFVYNVGDFPMALLSNGRYKSCLHRAVVNSTTRKBI LVDKLSPRLYPDFTWPMLLEFTQKHYRADMKTLEAFTNWLG 438 a 369 c 287 g 419 t	Query Match	474 GTCTCACAAACAGAGGGCTCAGAGGAGCACCAGGGGACCTGCGGCTATGCTAGCAGCTTTTTTTT	Db 645 CaladedTTTGAGAATTTTTTTTTTTTTTTTTTTTTTTTTTTTT
			CCGAGGGTGTACCCGGACTTCACGTGGCGGGGGGGCGTGCTGGACTTCACGCAGCGCACTA	mplete a, Tra eudic deae; an, M.J

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RESULT 14
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ORGANISM

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS TITLE

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Similarity
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Fivednustrokkendievptidiggelsgrsssykeaskivgracokhgfftyvneg
Vdanisbooytyndlefelblebkorokragescofassfigreskipwketlsfr
Fsarknsadivoyfbringebevlickyvobychamsrligipheligislgynreh
Fkeferennsimklivyprocypherigggrpheligggpheldpysliilhodnivgglevyvdnewr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toyomasu,T., Kawaide,H., Mitsuhashi,W., Inoue,Y. and Kamiya,Y. Phyrochrome regulates gibberallin biosynthesis during germination of photoblastic lettuce seeds
Plant Physiol. 118 (4), 1517-1523 (1998)
                                                                                                                                                      1115
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                                                          CAACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCG 1645
                                                                            996 AAATGGGAGATACAAGAGCTGCTTGCACAGGGCAGTGGTGAACAGCGAGACAAGAAA 1055
                                                                                                                                                                                                                                                             AB012203 1511 bp mRNA linear PLN 05-FEB-:
Lactuca sativa Ls200x1 mRNA for gibberelin 20-oxidase, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-MAR-1998) Tomonobu Toyomasu, Yamagata University, Reculty of Agriculture; Wakeba-cho 1-23, Tsuruoka, Yamagata 997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp, Tel:81-0235-28-2861, Fax:81-0235-28-2812)
1526 CATCCGCCTCGCCCCGGGGCGCTCGTCGTCAACGTCGGCGACACCTTCATGGCGCTCTC
                    1056 ATCTCTTGCTTTCTTTTTGTGTCCAAGAAGTGACAAGGTGGTGAGTCCACCATGTGAATT
                                                                                                                                                                                 CACGCAGCGCCACTACAGGGCCGACATGCGCATCCAGGCCTTCTCCGACTGGCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="2-oxoglutarate-dependent dioxygenase'/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ls20ox1; gibberelin 20-oxidase.
Lactuca sativa seed germination seed cDNA to mRNA.
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/db_xref="taxon:4236"
/tissue_type="seed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA37127.1"
/db xref="GI:4164141"
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KELVDENNPRVYPDFTWATFLEFTQKHYRADMNTLQAFSNWVEQKTSTT"
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                                                                                                                                                                                                                    12.4%; Score 309; DB 8; 58.1%; Pred. No. 9.3e-38;
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                                                                                  /note="28 a nucleotides"
321 c 295 g 41
                                                        /gene="Ls20ox1"
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- 1041 ITCIATGCCCAAAGAAGGATAAGGTGGTGAGCCCACCAAAGGAATTGGTGGATGAAATA 1100

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- QΣ

Search completed: March 26, 2003, 14:10:32 Job time : 5400.98 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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March 26, 2003, 04:18:30 ; Search time 4242.99 Seconds (without alignments) 15096.740 Million cell updates/sec
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2201
OM nucleic - nucleic search, using sw model
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Perfect score:
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1 cgtcgttcgttttgtgcatc......tagcttgtgcttttgctgta 2201 4109280 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: IDENTITY\_NUC Gaport 1.0 Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Scoring table: Searched: Sequence:

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database :

em\_htgo\_mus:\* em\_htgo\_other:\* em\_htg\_other:\* em\_htg\_mus:\* em\_htg\_pln:\* em\_htg\_rod:\* em\_htgo\_hum:\* em\_htg\_hum:\* em\_htg\_inv:\* em\_htg\_mam:\* em\_htg\_vrt:\* 9b\_htg:\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			с́Ф			SOMMANTES		
Result	ult No.	Score	Query Match		DB	Д	scription	
١	П	22	100	45999	1	AC096690	96690 Orv	, v.
	~	2201	100	4480	~	AC128647	28647 Orvz	sat
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	4	191.2	∞	1096	7	CNS08C7Q	31741	ω
	വ	90	ω.	4247	ထ	AP003627	3627	ß
	9	8	α,	5344	ω	AP003298	33298	Ø
ပ	1	8	ω.	6327	σ	AC078829	Ory	Ω
O	00	88	σ.	1382	a	OSJN00196	52998 Oryz	ß
	ð	8	ထ်	6485	(7)	AC092075	32075 Oryz	S
	10	8	ω.	5880	C)	AC104847	04847 Oryz	Sa
	11		α,	9969	C)	CNS07 YPX	13952	sat
υ	75	8	ω.	9155	Ø	AX429455	55	
O	33	82	ω.	4844	C)	AP004691	93	sat
	14	185.2	ω.	5449	(7)	AC120885	882	
υ	12	8	œ	7948	7	AP005305	305 Oryz	
	9	П.	œ	7246	~	AP005589	9 Oryz	
	11	83	ω.	2905	N	AP003754	54	
υ	18	83	φ.	3451	N	OSJN00134	344	Ø
O	19	83	∞.	4142	C)	AP005558	558 Ory	
O	20	183.2	ω.	2457	a	AP004078	)78 Ory	Sa
	21	8	ω.	7215	~	AP005492	192 Ory	ß
	22	183	ω.	3359	~	AC129227	_	S
	23	183	ω.	6017	~	AP005103	.03 Ory	Ć
O	24	r-1	ω.	7000	7	OSJN00133	343	Sa
O	25	82	ω.	2179	ထ	OSJN00064	609	
Ö	26	82	œ	4208	ω	AP004572	27	
	27	82	ω.	4943	7	AP005610	210	
O	28	8	œ	6667	7	AP005192	192	
	29	82	ω.	0737	N	AP005516	216	
O	30	82	œ.	0737	7	AP005516	216	
O	31	82	ω.	2248	7	AP003859	828	
υ	32	82	ω.	4828	7	AP004690	069	
Ö	33	181.6	ω.	971	7	CNS08C7X	AL731748 Oryza	
Ö	34	8	ω,	7002	7	OSJN00031	2290	sat
	35	8	ω.	5682	7	AC120532	533	
	36		ω.	6737	7	AP004236	1236	Sa
Ü	37	8	œ	6219	7	AP004160	1160	Sa
ပ	38	8	∞.	2910	N	CNS08C92	3379	ß
O	39	8	8	618	7	AP003896	68	Ø
O	40	8	ω.	5148	7	AC131343	343	w
O	41	180.4	ω.	5279	C)	AC120539	539	sat
O	42	5	ω.	8515	7	AP003454	3454	Ø
O	43	2	ω,	747	7	APG04704	004704	Ø
	44	20	ω.	3039	N	AP003565	3565	sat
	45	2	ω.	3777	7	CNS08C80	731751 Or	Sa

AC096690 145999 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBA0059G06, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 5 ordered pieces. AC096690.4 GI:20503077 HTG; HTGS\_PHASE2. Oryza sativa. Oryza sativa RESULT 1 AC096690/c LOCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE

ALIGNMENTS

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enthartoideae; Oryzae. 1 (bases 1 to 14599) Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K.,

REFERENCE AUTHORS

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Submitted (08-MAY-2002) The Institute for Genomic Research, 9712

Submitted (08-MAY-2002) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USB,

* NOTE: This is a 'working draft' sequence. It currently

* consists of 5 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be replaced

* the accession number will be general to the preserved.

* This sequence will be implied by the submittor.

* This sequence will be implied to the preserved.

* This sequence will be will be preserved.

* This sequence will be unknown length

* 71268 71367: contig of 2302 bp in length

* 71268 94779: gap of unknown length

* 122321 122320: gap of unknown length
Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, Q., Haas, F., Shi, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C. Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0059606 BAC genomic
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Submitted (22-SEP-2001) The Institute for Ge
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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As a factor of the contract of	Urya Sativa Ssp. Japonica cv. Nippondare Usunbouce19 BAC genomic sequence.  L Unpublished  E 2 (bases 1 to 244803)	S Buell, M. Direct Submission L Submitted (20-JUL-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20886. HSA	* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is	* arbitrary: Gaps between the contigs are represented as * runs of N but the exact sizes of the gaps are unknown.	* This record will be updated with the finished sequence * as soon as it is available and the accession number will * he preserved	36023: contig 36024 36072: gap of 36073 50777; contig	57039: 57088: 66062:	gap of	94296: contig of 3033 94345: gap of unknown 100470: contig of 6125 100519: gap of unknown	108149: contig of 7630 108198: gap of unknown 129485: contig of 21287 129534: gap of unknown	134076: contig 134125: gap of 141741: contig 141790: gap of	154796: contig of 13006 154845: gap of unknown 156853: contig of 2008 156902: gap of unknown	161078: contig 161126: gap of 179154: contig 179202: gap of	185368: contig 185416: gap of 188345: contig 188393: gap of 193528: contig	unknown length of 2516 bp in l unknown length of 3084 bp in l unknown length	204906: 204954: 210117: 210165: 212168:	gap of unknown length contig of 3914 bp in gap of unknown length contig of 2333 bp in	218559: gap of unknown length 221031: contig of 2472 bp in 1221079; gap of unknown length 226395: contig of 5316 bp in 1226443: gap of unknown length 229778: contig of 3335 bp in 1
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s; Pred. No. 0;
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unknown
                                                                        Location/Qualifiers
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/organism="Oryza sativa"
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                                                                                                            /db_xref="taxon:4530"
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Best Local Similarity 100.0%;
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166590 CGGTGGAGGAGGCGATGGAGCAGCTAGTGAATGTGGACCACAACTTCTACGCCTTCAGAG 166649
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryacae; Oryacae;
Oryacae; Oryacae; Oryacae;
Buell, C.R., Tuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K.,
Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B.,
Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.,
Utterbach, T., Reläblyum, T., Yang, Q., Haase, B., Sub, B., Peterson, J.,
Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
Ouyaca sativa ssp. japonica cv. Nipponbare 031754_E06 BAC genomic
                                                      166710 TCGTCCCCAAGGGAGACGCCATCTCCACAAGGAGACCATCCCCAACTCTGACCACCACC 166769
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Submitted (1-DEC-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 207376)
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ON MAT 5, 2002 this sequence version replaced gi:18767486.

* NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC104433 207376 bp DNA linear HTG 02-
Oryza sativa chromosome 3 clone 0J1754_E06, *** SEQUENCING
PROGRESS ***, 34 unordered pieces.
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                                                                                                                              1921 ACCCTCCCTTGCTGCCTAGCCTCTACACCTCCTGCATCACCATCCTCATTTGCTAATTA
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10151: gap of unknown length
13105: contig of 2954 bp in length
13154: gap of unknown length
20540: contig of 7386 bp in length
20589: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 167010 TATTTCTGGAAGCTGCARGTATAGCTTGTGCTTTTGCTGTA 167050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2161 TATTTCTGGAAGCTGCATGTATAGCTTGTGCTTTTGCTGTA 2201
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Direct Submission
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	Best L	Best Local Similarity 99.7%; Pred. No. 0; Matches 2045; Conservative 3; Mismarches 2: Indels 1: Gans 1:	Dp 2	1623 TCAAATGKTAGTCGAAAAGTCAATGGTGTCATACA
QV 4G		GIGCATCCATCCAGAATTCGTTCCAGATCCAGCCAGCCAGCC	Ω <sub>γ</sub>	1081 ATAGCTACAGTAGCACAGTCATGATAAAGTAGTATA. 
8 6 6		120	Qy Db 2	1141 TOTGTGGAAAAATAAAGATGGGAATGGAATGGAA1 
, U A		GCGAGAGCAGCATTGTTCTTCTTCTTCTTATAGTGGGGGAATAATGGCTCCCG 18    CTGAGAGCAGCATTGTTCTTCTTCTTCTTATAGTGGTGGGGGAATAATGGCTCCCG 18   CTGAGAGCAGTGGTTCTTCTTCTTCTTTTAGTGGTGGGGGAATAATGGCTCCCC 18   CTGAGAGCAGGAGCATTGTTCTTCTTCTAGTGATGGTGAGAATAATGGTGAAAAATGGTGAAAAAATGGTGAAACACCCC	Oy Db 2	1201 GCTGCAGCTGAATGAGAAGCTGAAGGAGCACATCC 
, yo du		CACCACCACGCAGCAATGGCCCTCGCGCCTCCTTCCCATCACCATGCACATGCACATGCACCATGCACATGCACCATGCACATGCACCATGCACATGCACCATGCACATGCACCATGCACATGCACCATGCACATGCACCATGCAATGACAATGCAATGACAATGCAATGAATG	DD CV	1261 GAAGCACAGCTTGTGAAGGAGTGGACGTGC 
. දින් දින්	y 241 b 22403	TCAAGCAGCTGCAGCTCCCTCGTCTGTCTCCGTCTCCGTCCCCTCCGGTTTCC	Oy Dp 2	1321 CAGCCGAGGTCCCAAGATTTGCAGGTGCGAGATCP 
. ~ da	QY 301 Db 22343		(1)	1381 CATCGGGGGGGGGGGGGGGGGGCCACCTACC 
σд	Oy 361 Db 22283	GCAGCAGCGCCGTGTCGTGGGGATGTCGTGGGCCCCTCTCCTCGGTCCGCCTCA 420	QY Up 2	
U D	Qy 421 Db 22223	TTATGCAGGGCCGCATALLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY Db 2	1501 GACCAAGCCCCCGTCTCCGACTGGCCGCCATCA? 
υ <u>α</u>	Qy 481 Db 22163	TGGAATTTCCTTCGTTCATATTATAAGGTTTTCTAGCATTACTCATATTCACATATATA 540 	OY Db 2	1561 CCAGGCCCAGCTCAAGGATCTGGAGGAGGCCGTCC 1111111111111111111111111111111
σд		TATATATGATAATATTCTAGATTCATTATCATATATATAT	QY Db 2	1621 CACCAAGGTCTGCAGTCTGATGCATGATCAALGC2 
OI A		TCTTATAACCTGAAACAGAGGAGTATAATAATTCGGTAATGGAACTAGAGTATTGTF 660	Oy Db 2	1681 aattaatgcaactgtgaatgcaggtggtgcgcack 
, , ,		TATTAATTGGACCTTAATACTAGTAAATTCAACGAAACTACATCTTTAT [	QY Db 2	1741 CGGTGGAGGCGATGGAGCAGCTAGTGAATGTC 
5 1	Qy 721 Db 21923		QY Db 2	
<b>У</b> П	Qy 781 Db 21863	ATTATTACAAAACTAACTGTATACCGGTTGCAACGGAATAGTAATATGGACTATTACTT	(2)	
5 1	Qy 841 Db 21803	A ATTACTACCTCCATATTTAATGTATGACGCGGTTCACTTTTGTCCAACGTTTGACCAT 900	QY Db 2	1921 ACCCTCCCTTGCTGCCTAGCCTCTACCTCTCTCTCTCTCT
, I	Qy 901 Db 21743	TCGTCTTATTAAAAAAATTAT 	6	TTTCTATGCTTG
0 1	Oy 961 Db 21683	1 Caaataittittaagcatgacataacattitcataittgcaaaaaaaaaa	Qy Db 2	2040 GAGAGGTCTTT 2050 20603 GAGAGGTCTTT 20593
J	Qy 1021	1 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATATGGG 1080	RESULT 4 CNS08C7Q	T 4 C70

CCAAGGTGTTCGAGATGCCGCCGCTGT 1740 GGAGACCGACGTCCGCCACCTCAAGGG 1500 TGGACCACAACTTCTACGCCTTCAGAG 20844 CGCCAGCATCGACCTCGCCTCCTCCAT 21204 21324 CATTAAAATACGGAGGGATTATATGGG 21564 ATGAAAAGCGTACGTGCGTGGCGTGGC 21444 CGCCAGCATCGACCTCGCCTCCTCCAT 1440 ATTGCTCGACACAACACGACGACGC 1560 CGGCGCCGAGGACGACGCTGCT 1620 TGGACCACAACTTCTACGCCTTCAGAG 1800 AGAGGAAGGAGGCTTCGGTCTCA 1860 AGACCATCCCCAACTCTGACCACCACC 1920 TGCATCACCATCCTCATTTGCTAATTA 1980 ATGAAAAGCGTACGTGCGTGGCGTGGC 1200 CGAGGAGAGGCGGGGAGAGCAGTGGC 1260 SCGCCTCTCCGCCGCGGTGGCGAGCT 1320 SCGCCTCTCCGCCGCGGTGGCGAGCT

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95874 TIATAGCCTCCATATITTAATGTATGACACCGTTGACTTTTTGTCCAACGTTGACCATT 95933
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The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
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   HTG 29-APR-2002
                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-APR-2002) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Web : www.genoscope.cns.fr) IMPORTANT\colon This \ sequence \ is \ unfinished \ and \ does \ not \ necessarly \ represent the \ correct \ sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 2400: contig of 2400 bp in length 2401 2500: gap of 100 bp 2501 8509: contig of 6009 bp in length
                                  Oryza sativa chromosome 12 clone Monsanto-031298_D03, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 110969;
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2400 bp contig from 1 to 2400
5450 bp contig from 2501 to 8509
5450 bp contig from 8610 to 14059
11245 bp contig from 14160 to 25404
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8610 14059; contig of 5450 bp in length
14060 14159; gap of 100 bp
14160 25404; contig of 11245 bp in length
25405 25504; gap of 100 bp
25505 110969; contig of 85465 bp in length.
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linear
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8610 14059; contig of 5450 bp in length
   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa chromosome 12 sequencing Unpublished
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a 25445 c 24509 g 30381 t
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                                                                                                                                   AL731741.1 GI:20160276
HTG: HTGS_PHASE2; HTGS_ACTIVEFIN.
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/sub_species="japonica"
/db_xref="taxon:4530"
110969 bp
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Matches 222; Conservative
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Direct Submission
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842 TTACTACCTCCATAITITAAIGIATGACGCCGTTCACTTTTTGTCCAACGITTGACCATT 901

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Sasaki,T., Matsumoto,T. and Yamamoto,K.

Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone=10455984

Lublished Only in Database (2001)

RS Sasaki,T., Matsumoto,T. and Yamamoto,K.

Direct Submission

AL Submitted (17-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tasaakidenias.affrc.go.jp, URLihtp://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7466)

On Aug 24, 2001 this sequence version replaced gi:14575596

Genes were predicted from the integrated results of the following:
GENGSANIO, BLAGYNIO, BLAGYNIO, OBLAGYNIO, BLAGYNIO, BRAGINIO COCTOBER 1998 VERSION OF AN AGRICH AGAINST REPROBLEMENT ROBER OF A GENERAL BLAGYNIO, BRAGINIO CONTESPONDING A GENERAL BLAGYNIO, BRAGINIO CONTESPONDING A GENERAL BLAGYNIO, BRAGINIO CONTESPONDING BASED OF A GENERAL BLAGYNIO, A 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLN 21-MAR-2002
chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/denomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0459B04.

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzae, Oryzae, Oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
                                                                                             95934 CGTCTTATTCAAAAATTTATGTAATTATCATTTATTATTATAACTTGATTCGTCATC 95993
                                                                                                                                                                                                                                                                                                                                                                                                                                                  95994 AAAIGITITITTAAGCATGACATAAATATITTCATATITGCACAAAAATTTGAATAAAAC 96053
                                                                                                                                                                                                    AAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA,------AAAAAAAC 1014
                                                                                                                                                                                                                                                                                                                                                                                               1015 GAATGGTCAAATGTTÄGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTA 1074
CGICTTATTAAAAAAATTATGTATCTATTATTTATTATTATGACTTCATTCGTCATC 961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group) genomic DNA, PAC clone:P0459B04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP003627.3 GI:15290128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96114 TATGTGTTAGCT 96125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1075 TAIGGGATAGCT 1086
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STYLRRHSLQYGATFFFRGORIWEAVMAELLPKGLARAKOGRHFWBKDLRKRFPGCSS
BENDEGOCFFFORDERYKGITTPMFILNPAYDVWQTVAEAVGDWFFDRREVKEIDCBYPCN
PTCENVYLEQPEYGE9
JOIN (65394. . 65405, 65622. . 65777, 66253. . 66420, 66764. . 67036)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNOESAPSKITTOSROPSADVARSVLIKLY TOMTKARDLIIANIGIHAHLLEPMIVENA
SLIEKSETVHSYMANBYGSSADBORATESBOBORMEROBIVMASALSCLFYBYCDG
GKIIRKNGGLDIRVIKTULEISVEHOWAKVYHSKIICMLTWALXVSOBORDADIT
HFLPDOLINGVYLICLESTRANSREKRDLFYLFODYVLHQINBTFLAGGISTYTY
DDAOPLASILACADAPEAFYISVKHGVEGVGDMLRKAISSALSGSTEYEQINVLLIDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OMCAACTLAICCHSKPNPKTLLLHPPACPFCRTTISRLVVATTNSNKTNSRRRSRSRS
SSFKGGLGSAMGSFSRTGRGSGRLVVDGSSYGELANKPDHPFSSYAAAAICDT"
complement(join(56259. 56384,57157. 57234,57351. 57401,
57530. 57550,58700. 58869,59089. 59518))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join:56259. :56384,57157. :57234,57351. :57401,
57530. :57550,58700. :58869,59089. :59518))
/gene="P0459B04.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MPPLFSAPALHRRRLLRHAAAFALVLLAVALLFILLVHPRSLGT
PSPSPSYGHRLPTLVDLTLVHGAKEKGAVCLDGTPPGYWLPGFGDGSNKWLLHLEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWCRNRTSCDHRKKTSLGSSAYMETRVEFVGILSDDKAQNPVTIPYTPHFTSPHFLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAVQVQESKRDYIANPSTIDMAYNVLIDHALAERDRSPAVVPKC
VSLLKTYLIRYTPRVQTLRQIDLFCANTIAKCEPLGTQRSSSASPHSSVAAPPITNFA
SPSLVKSLNYVRSLVARHIPKLSFQPIGHSVAPTSTKQSLPSLSSFFNKSLVSQLTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id~"BaB63825.1"
/db_xref~"GI:15290134"
/translation="WGHGLSCSRDTDEYDLFRAAQLGDIHALSALLAADPALARRATV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YDRFTALHTAAANGRLGVLSMLLDRDGDVDVLSRKRGFPLMVAAMRGNTECVVRLLRG
GANVLTFDSPRARTCLHHAAYYGHAECLQATLGAAQAQGPVAASWGFARFVNVRDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AWGADRLQRDSAGRIAYAVAMRRGHRACAALLNPAAAEPIVWPSPLKFIGELEADAKA
LLBAALMEANREREKRILHGSDINIKGGDEEEESEDEBEACNICFEQACSMEVKECGH
                                                                                     /translation="mSCCGGNCGCGSSCQCGNGCGGSIDRCNSNLTIDICRCKYSEVE
PTTTTFLADATNKGYVWCCFRRIRDGGGERQLRLQHLQVRHQLRLLLLQLQLGLEETYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STKESSNDFADLQDFHTQGFLEVGAAALLVGDMEAKINDQQWKYSFIQDFPDIDLLQP
STSTASTFASSQSHLKAITASKRMKSGPNQVCEQQPLKINPABISEVIAEVCSETTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRKLDGTVSTFSRIDTEFAYMIQVTKSYKCFSSIRDGHEDADVALRARLCWATLHSLL
NSQISSYRHHGYIMLVELLLSEISEETDGSIWSKIQKLQDEIEVAGSQDLSSSEVSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VCLLCGLLKSKHNFIRWGFLYVLDKFLMRCKLLLDDNDMQEHTVADHSKHRLDKAFAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDIMNSALLLIVVQNNETDHINILKMCDMLFSQLCLRLPSSNVMHMGGLQSLGQLFGCT
TKNIESHLETLASHQNVGNKNFCRSEFILQDISVNQTAQFTLLSEFSMAALLLRGLAIA
                                                                                                                                             HPIHHLINELPVPLHMPCTSYLACMQVLNLLLAS"
complement(join(39014. 39084,40410. 40797,41574. 42182,
42726. 43001,43610. 43798,44035. 44145,44725. 444905,
45677. 45853,4074. 46958,47100. 47606,47693. 47743,
47836. 47915,48207. 48236))
                                                                                                                                                                                                                                                                                                                                      complement(join(39014. 39084,40410. .40797,41574. .42182,
42726. 43001,43510. .43798,44035. .44145,44725. .44905,
45677. .45583,46704. .46958,47100. .47606,47693. .47743,
47836. .47915,48207. .48236))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           altnmdiveskeshapsdlissatekadggepaddtkyisfdilnwrwhvygerqasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATPLHLAARHARASCVRLLLDKGAIVSAPTAVYGFPGSTALHLAARAGSMECIRELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMQLVARVPTSLFFWPLMQLEGAASDDIALGIAVGSTGSESPVTCKLITGSKRCGYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to Arabidopsis thaliana chromosome 3, T2E22.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="putative receptor-like kinase Xa21-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="P0459B04.7"
/note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB63826.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/protein_id="BAB63824.1"
/db_xref="G1:15290133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:15290135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53255. .54595
/gene="P0459B04.8"
53255. .54595
/gene="P0459B04.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(29581 .30063,31083. ,31412,32281. ,32354,32618. ,32708,
32819. ,32911)
/gene="P0459B04.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(29581 .30063,31083.31412,32281.32354,32618.32708,
32819.32911)
/gene="P0459B04.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="Bab63821.1"
/db_xref="G1:15290130"
/translation="MATTRSFLPPPFIALSSNPRPTILAPTPNPRPRRRNSLAICSAS
ASGDPSPPBAEGGGNPLIALMRRILHPLGDYGFGKRSVWEGGYGLFWYSGALLALA
LAWIRGFQLRARFRYQAVFEFTQAGGICVGTPVRLRGTWYGNVYNDSSLKSIDAY
EVEDDKIIVPRNSVVEVNQSGLIAMETLIDITPROPLPTPSYGPLDPDCSKEGLILCDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAHSGFSGSLTSPRFDLAVDMGHPFLNRTVDGFLKIGAKNAMVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ERMKGQQGVSLDALVGIFTRLGRDMEEIGVHKSYKLAEKVASIMEEAQPLLSRVRDSD
                                                                                                                                                                                                                                                                                                                                                                                                                                      AVCVŠKAQGFDKIPGSDHEYIDVIANSDFEYRLIIDIDFRSHFEIARAVDSYDSLLNS
LPVYVGTLPRLKQFLHVMVDAAKWSLKQNSMPLPPWRSLPYLQAKWHSKYERIDHJ
BQDFHSTASDHALCIGHLKRLKSSLQSELDTERLLAMPIKTDWKRRAKFERRRRSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKDVEIIAKGLADASGDLRRLKSSMLTPENTDLIKQSIFTLIFTLKNIESISSDISG
                                                                                                                                                                                                                                                                                                                                                /translation="MLLAKELGLSPPAAVTPRRRPPPARVPASPSGGSPVAVGDLWLR
                                                                                                                                                                                                                                                                                                                                                                             TKGAGGGGGFGSASHESEMDLAMLYTDFLENGGTGGADSRASSDSDSALSDHLADNT
SIYKQGGDEKENELLSMYHSLLFSIHESDLLAFKRGQCSASCIRHLLVKLLRYSGYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(36642...36706,36726, .36840,36947, .37177)
//gene="PO459804.6"
/note="contains ESTs AU031375(E61447),AU029988(E50438)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to Arabidopsis thaliana chromosome 3, MQC12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15732. .16972

/note==75 I_RR"

/note==75 I_RR"

/gene="0455904.2"

17059. .23204

/gene="pot/55904.2"

/note="pot/bably inactive due to frameshift(s) in CDS

probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note~"probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar to Oryza sativa chromosome 6, P0644B06.8"
                                                                                                                                                    /note="contains EST D47569(813151)
similar to Arabidopsis thaliana protein F1216.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAVTGALVSAASNSHRQNVVKNAITGGAIATAAEFLNYLT"
join(36642. .36706,36726. .36840,36947. .37177)
/gene="P0459B04.6"
                             .7448,7556. .8040)
                                                                                         .8040)
                join(6392. .6700,7232. .7448,7556.
/gene="p0459B04.1"
join(6392. .6700,7232. .7448,7556.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTGDDATRRNIKLLIKSLSRLL"

join(33620. 33733,35242. 35382)

join(33620. 33733,35242. 35382)

join(33620. 33733,5242. 35382)

/gene="P0459504.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0459B04.3"
complement(23838. .2697£`/gene="P045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0459B04.3"
/note="proh-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAB63822.1"
/db_xref="GI:15290131"
                                                                                                                                                                                                                                                                                 /protein_id="BAB63820.1"
/db_xref="GI:15290129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similar to polyprotein"
                                                                                                                         'qene="P0459B04.1"
/clone="P0459B04"
                                                                                                                                                                                                                   unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="3' rm-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTR"
                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pseudo
27447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /bsendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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                                    gene
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This sequence of P0698H10 clone has an overlap with P0518C01 (DDBJ: AP003277) clone at the position 1 to 80,700 of 5' end and with P0459B04 (DDBJ: AP003627) at the position 103.851 to 153,449 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB89859.1"
/db_xref="G1:20160923"
/translation="MEBEBEBEBEEKERKKERVVELISMEDERWKLSSSKGRSKSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WFERRLSFRLRSCCCFFFFLLVVVVVVVIAMMYQTQAVGTNDIDQAGETWFLDEGPAS
RAEEQRPAGATCICSLLARAYCRPCLRWHACTTYYCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLAKQCNAMQSDQIFWRMKDEVTRALGRILSGVGRVTNDTRLAW
LAMRYFSANNPLLAPIFFGKLKQHCWMADLLLKRGINSHSAYPFYAQELETANHILLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLLLQRTYEATKELKNKLASYLFLIDRFFFFFFFFFFFFFFFTVSLTSCVYRDIPGLPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(26367. .26488,26778. .26908,27759. .27874,
28412. .28548,29329. .29416))
/gene="p0698H10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MQTLMSVFVIIIGNYTAIDWITDIVIFWIGVGTWHLKRCQTVKL
XIAAPLIFYIVMALFGFIKQLIBYNIIAFCHPSTVFRFGKSTRETWTKMIBALGFGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MHAGTDRFKFSCDVLLAANSQDTLCTVMLAWRRASHAYVVLSSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(32396. 33552,33673. 33814,34064. 34197, 35201. 35214,36092. 36171))
/gene="P0698H10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .16340,16376. .16523,17419. .17541,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .26908,27759. .27874,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(4643. .4651,4721. .4846,4888. .5021,
8292. .8312,9406. .9448))
/gene="p0698H10.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .4651,4721. .4846,4888. .5021,
                                                                                                                                                                                                                                                                                                                  /organism="Cryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
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complement(join(28367. .26488,26778. .2
28412. .28548,29329. .29416))
/gene="P0698H10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(11376, 11773,12758, /gene="P0698H10.2"
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(11376. .11773,12758. /gene="P0698H10.2"
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35201. .35214,36092. .36171))
/gene="P0698H10.5"
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/gene="P0698H10.3"
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/codon_start=1
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8292. .8312,9406. .9448))
/gene="P0698H10.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="P0698H10"
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                                                                                                                                                                                                                                             FEATURES
    /gene="P0459B04.10"
join(65394. .65405,65622. .65777,66253. .66420,66764. .67036)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the identified CDNA Sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein.' A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 1,
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clone:P0698H10.
                                                                                                                                                                                                                                                                                                                      44550 AAACGAATGGTCAAACGTTGGTCGAAAAGTCAACGGCGTCATACATTAAAATACGGAGGG 44609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA-----AAAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                           838 CITATTACTACCICCATATTITAATGIATGACGCCGTICACTITITGICCAACGITTGAC 897
                                                                                                                                                                                                     Gaps
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Direct Submission
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0696H10
                                                                                                                    DB 8; Length 142475;
                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aruus298 153449 bp DNA linear Orysa sativa (japonica cultivar-group) genomic DNA, PAC clone:P0698H10.
                                                                                                                                                                                                 0; Mismatches 24; Indels
                                                                                                                                                                 Pred. No. 1.1e-22;
                                                                                                                    8.7%; Score 190.6;
87.7%; Pred. No. 1.1
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2 (bases 1 to 153449)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP003298.3 GI:20160921
                                                                                                                                                                                                     Conservative
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                                                                                                                                                             Similarity
                                                                                                                                                                                                 Matches 222;
                                                                                                                        Query Match
                                                                                                                                                                 Local
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AP003298
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SOURCE
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HISKQPAFDHPLLKNHTIQPSGMYGBAARPFTQTWNGMGEKCPDNTVPIRRTKEEDVM
                                                                                                                                                                              RAISŸAIFGKKTHGSHHPŘLAGYTDGHHQYGVÄSATĞDANYYGTKAITNIMQPTIATS
GDFGILAQÍMISAGSYQNKDLNYTEAGWOYYPALYDDEKTRPIYWTRDAYDQTGCYNL
ACSGFIQTNTVIGGSTSPVSIYGEQUYEYDYLVWKDLAGGNWWLQVQGKYVGYWPSSI
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NGVSLIAPLPNYINVWHGSSSTTSWGTYIYYGGSGCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Bukaryota; Vinidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 162279)
Buell, C.R., Yuan, Q., Moffat, K.S., Hill, J.N., Burr, P.C., Hsiao, J.,
Zismann, Y., Pai, G., Bowman, C.L., Fulli, C.Y., Vanken, S.E.,
Bowman, C.L., Craven, B., Utterback, T.R., Khalak, H., Feldblyum, T.V.,
Quackenbush, J., White, O., Salzberg, S.L. and Fraser, C.M.
Oryza sativa chromosome 10 BAC OSJNBa0026012 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 148220 CITAATACTACCTICATATITTAATGTATGACGCGGTGACTITTGTCTAAACATITGAC 148279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 148340 CATCAAATGTTCTTTAAGCATGACATAAATATTTTCATATTTTGCACAAAAATTTTGAATA 148399
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Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
5 (bases 1 to 163279)
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Submitted (27.FEB-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
4 (bases 1 to 163279)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                838 CFTATTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGAC 897
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                                                                                                                                                                                                                                                                                                                                                               Length 153449;
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                                                                                                                                                                                                                                                                                                                                                               DB 8;
                                                                                                                                                                                                                                                                                                                                                            Score 190.6; DB 8 Pred. No. 1.1e-22;
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//gene="P068BH10.7"
join(42534. .42746,42822. .43280,43389. .43616,44080. .44259,4335. .44655,44769. .44834,45256. .45308,45405. .45491)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(47688 .47948,48328. .48393,48479 .48576,48699. .48736,48809. .48736,48896. .498736,49896. .49414,49903. .49552,49349. .49414,79603. .4965810,8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .48736,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKTPHKVLDAPSLQDDFYLMLVDWSSQNTLAVGLGNCVTLWSASNCKVTKLCDLGPRD
SYQAVHWTREGSYLALGTSLGDYOLWSSRCKTRIRMGGHQTRTGVLANSSRLILSSGS
RDKILLQHDIRVPSDYILSKRSGHRSSRNHVCASSDSFRGQVCGLKWSHDDRELASGGND
NOLLWWNORSQQPTLRLTEHTAAVRA I AWSPHQOGLLASGGGTADRCI FERWINYNGNN
LNSYDTGSQATCEHSWYFPKPNHGVEVPIYVKGCYSNWTHAASALPCNYTTIVTGAGD
                                                                                                                                               STTSPPACLRRRILVSSPMRLVGHTTVHGRPRLHRPAGLRRRLVFPPARLAYYAAAI
GHLRLHRRPTSVAADWCLRLHGWPIMPPLLGVYDFTAGLPPSPPSGASAYTAGLLCRR
CWASTTSPPACLRCRRVVPPPFTRLAYYAAAVGRLHRRPASVAADWCPRLYGWLVTP
                                                                                                                                                                                                                                   PFMGVHVFADRLARAAADWCFRLHGWPLMPPLLIDVYDFTAGLPPSPPTGVLAYTVGWS
HHRSWASTSSPTGWPSPPPTGVSAYTASLLCRCCWASTTSPLACLCRRRLVFPPTRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEAEEEDEREYFAAAAADDQLQVEAPCGRRRRESMVNKLISTVYSGPTISDIESALSF
TAAGDHQLLADGHNFAASSCSPVVFSPEKTLSKTMENKYTLKMKSCGNNGGLADDGYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WRKYGÓKSIKNSPNPRSYYRCTNPRCNAKKOVERAVDEPDTLIVTYEGLHHYTYSHF
LHSTESSESSTTTOQOLQPQWATNOKKRPKLHHELLINDPPPPPPPPEMTYMAIN
OSFSIQOQHDDOLQPADPLMVQAPPDCYNINGSSSSGTMASLDDDDAAGAG
GLLEDVVPLLVRRPPPPICNNNYYYSPATTCTSDNEYGSSASASPSSSVSVSWYTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MIMGRPAMQREYNGYSGGGPTYRGRQLVLEKVGDLPTPTKVTVA
TSSPLITLILIVVVVVVGGASSLDYPAPAPPRPTANDYPAMAGGLRLDPAYASPARLILD
VPKTPSPSKTTYSDPRTPCRSSSRLHNFALLDNDRASPSSTTDDAPYSKLLRABIFGP
DSPSPAPSSPNTNLFRFKTDHPSPKSPFAASAAATAGHYDCTAGGAESSTPRKPPRV
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PVLRNILLSLPIRKYVYFNCFDQYFTNGDRIHASRALKRIGIEDCFERYYCFETINPS
PILCKFNIDAMRQALKVASINPKTSILFDDSARNIQAAKLIGMYTVLYGTSERIKGAD
                                                    /translation="mmrdiggsnptrtwrarasttdnyriirwsgdrssgifscvdlv
SVGGDQaravddalmhrdflrvllldmwwlslalqldrsviymldtlggrraydgfrr
Liliaalrpklidahdvskprhhdiavlyvyrtdrplrpppigvsactagilcrrcwa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MQESREYWRDGGDVVGEELLREILDETAAVHSNSNSNSNSNSNSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MECESNYSKEQRINGDSLVFDLDDTLYPVTSGIGADVVRNIQAY
                                                                                                                                                                                                                                                                                              YYAAAVGRLRLHRRPASVAADWCPRLYGWLVTPPFMGVHVFADRLAFAAADWCFCLHG
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join(52973. 53089,53413. 53871,53703. 53789,53938. 54
54208. 5431,56578. 55731,55862. 56002,57568. 57924)
Gene="P0698H10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jóin(47888. .47948,48328. .48393,48479. .48576,48699. .4
48808. .488949,48960. .49081,49175. .49252,49349. .49414,
49503. .49658)
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                                                                                                                                                                                                                                                                                                                                             join(40057. .40430,40631. .40783,41168. .41861)
/gene="P0698H10.6"
join(40057. .40430,40631. .40783,41168. .41861)
/gene="P0698H10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative cell cycle switch protein"
/protein_id="BAB89864.1"
/db_xref="G1:20160928"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB89865.1"
/db_xref="G1:20160929"
/protein_id="BAB89862.1"
/db_xref="G1:20160926"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB89863.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GI:20160927"
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/gene="P0698H10.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSPCIDMAILSNIF"
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complement(join(<36223. 36759,36892. 37157,37825. >37996))
/gene="OSJNBa0026012.6"
complement(join(36223. 36759,36892. 37157,37825. 37996))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="0ryza sativa gene, repeat sequence Micropon-4 gi|4586620|dbj|Ab010112.1|Ab010112" complement(41839. .56317)
/rpt_family="0ryza sativa gene, repeat sequence Micropon-4 gi|4586620|dbj|Ab010112.1|Ab010112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unuplement(join(36223. 36759,36892. 37157,37825. 37996))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41836. .56291 /rpt_family="0ryza sativa gene, repeat sequence Micropon-4 gi488650{db}|AB010112.1|AB010112" /rpt_family="(TR84) /rpt_family="(TR84) /rpt_family="(TR97)" /rpt_family="(TR97)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Oryza sativa gene, repeat sequence Micropon-3 gi|4586621|dbj|Ab010113.1|Ab010113"
complement 42556. .42578)
/rpt_family="AT_rich"
complement 443917. .43952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Oryza sativa gene, repeat sequence Micropon-4
gi|4586620|dbj|AB010112.1|AB010112"
41839. .56317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGTTRAVVGMRKTLVFYLGRAPNGQKTTWVMHEFRLETPNSQPKEDWVLCRVFDKKKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MAGLREMESTLPPGFRFCPSDEELICFYLRNKVANHRVASGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVDLHAREPWELPEVAKLTAEEWYPFSFRDRKYATGSRTNRATKTGYWKATGKDRIVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STIEAEGGGSSGSDLFIPGATDGSTDPSSPTTMAPLLGSSPDPTVVDRPDHRSAAVPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMVLMQGGGDQMISGSGVHCSNNDNSGSSSALLNLTMLQYSFLEHRPTGDDMAVGAHF
                                                                                                                                                               /translation="meagaraavkealaalvhHpDbarrraadrwLgoFQHTLDawQv
ADSLLHDESSNWETQIFCSQTLRSKVQRDFEELPSEARPLQDSLYALLKKFSKGPQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="similar to NAM GB:CAA63101 GI:1279640 (Petunia x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative NAM (no apical meristem) protein"
/protein_id="AAK13151.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCQGGNNDATMALGMOREEEGMGEIIEMEPAWRQGGSNCVYRDELYF"
complement(40273 .40295)
/rpt_family="ar_rich"
1856 .5629"
                                                                                         transport receptor'
27721. .27783,27886. .27963,28907. .29035))
/gene="OSJNBa0026012.16"
                                                                                                                                                                                                                                                                                                                                                                                                    Complement(34290. 34356)
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34452. 34525
/gene="05JNBa0026012.tRNA-Asn-1"
34452. 34525
/gene="05JNBa0026012.tRNA-Asn-1"
                                                                                   /product="putative nuclear/protein_id="AAK13152.1"
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/rpt_family="(TGGGGG)n"
complement(29966. .30049)
/rpt_family="AT_rich"
33907. .33948
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/note="simil-
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4436, .444Fc
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/rpt_family="(TA)n"
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/rpt_family="(GA)n"
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/rpt_family="AT_rich"
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                                                                                                                                        /db_xref="GI:13129498"
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                                                                                                                                                                                                                       VRTQICIAMAALAVHVPFG"
29166. .29196
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                                                                                                                                                                                                                                                                                                                                                                                           Genes were identified by a combination of several methods: Gene prediction programs including Genscan and Genscan+ (Chris Burge, http://ccr.081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), Figenesh (http://genemark.biology.gatech.edu/GeneMark/), Figenesh (http://www.softberry.com/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tig:.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgishtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by protein surel. edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://encome.maki.ar.edu/eddy/tRNAscan-SE/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(<26795 . 26803,27038 . 27076,27396 . 27443,
27721 . 27783,27862 . 2783,28907 . .>29035))
/gene="CSJYMBOODS602 .16"
complement(join(26795 . 26803,27038 . .27076,27396 . .27443,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /hote="similar to nuclear transport receptor GB:CAB42643
                                                                                                                                                         Direct Submission
Submitted (03-JUL-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
On Jul 3, 2002 this sequence version replaced gi:13129494.
Address all correspondence to:rice@tigr.org
                         Direct Submission
Submitted (29-Aug-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
6 (bases 1 to 163279)
                                                                                                                                                                                                                                                                                                                   BAC clone OSJNBa0026012 is from Oryza sativa chromosome 10 The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This BAC overlaps with rice BAC OSJNBb0044B19 (AC078893) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html)
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complement(1575. .1683)
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/rpt_family-"AT_rich"
complement(13043. .13081)
/rpt_family-"AT_rich"
complement(16661. .16686)
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/gene="OSJNBa0026012.16"
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complement/for
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/rpt_family="Ar_rich"
complement(5159. .5181)
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/db_xref="taxon;39947"
/chromosome="10"
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Location/Qualifiers
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                                                                                                                                Buell, R.
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                                                                                                          REFERENCE
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ACU92075 164852 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBa0017N12, *** SEQUENCING IN PROCRESS ***, 9 ordered pieces.
                                                                                                                                                                                                                                                                         were identified by a combination of several methods Gene
prediction programs including Fgenesh (http://www.softberry.com/),
genscan (http://CCR-081.mit.edu/GENSCAN.himl), GeneMarkEMM
(http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean
Eddy, http://genemark.biology.gatech.edu/GeneMark/), tRNAscan-SE (Sean
Complete sequence against NCBI none redundant protein database (nr)
(ftp://ncbi.nlm.nh.gov/blast/db) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
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                                                       Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC clone: OSJNBb0020011.
On Jul 12, 2002 this sequence version replaced gi:17998510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD 101222 TACTATCTCCATATTTTAATGTATGACGCCGTTGACTTTTTGTCCAACGTTGACCATTC 101163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 101162 GPCFTRATFCAAAAAFTTATGTAAFTAAFCAFTTATTTATTAAFGACTTGAFTAGFCATCA 101103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 101102 AATATTCTTTAAGCATAACATAAATATTTTCATATTTGCACAAAAAATTTGAATAAAG 101043
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                                                                                                                                                                                                                                                       NOTE: This is a PHASE2 sequence. Gaps are shown by nnnnn. Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             903 GTCTTATTAAAAAAAATTATGTATCTATTATTATTTATTATGACTTGATTCGTCATCA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843 TACTACCICCATATITIAAIGIATGACGCCGTICACTITITGTCCAACGTITGACCAITC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
     HINA. E-mail enquirles: bhan@ncgr.ac.cn. Clone requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%; Score 188.6; DB 2; Length 113825; 82.0%; Pred. No. 2.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 others
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88557 113825: config of 25269 bp in length.
Location/Qualifiers
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/clone_lib="CUGI-OSJNBb"
25501 c 25985 g 30469 t
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                                                                                                                                                                   ...-- Summary Statistics
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∕organism="Oryza sativa"
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/db_xref="taxon:4530"
                                                                                                                                      Web site: http://www.ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /variety="Nipponbare"
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                                                                                                                                                                                                Assembly program: phrap
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                                  ohan@ncgr.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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AC092075
                                                             REMARK
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                                                                                                                       Complement(54472. 54210)
//rpt_family="Ar_rich"
complement(55251. 55381)
//rpt_family="Ar_rich"
complement(55243. 55320)
//rpt_family="Oryza sativa gene, repeat sequence Micropon-3
gij4586621[db]|Ab010113.1|AB010113"
//rpt_family="Oryza sativa gene, repeat sequence Micropon-3
gij4586501[db]|Ab010112.1|AB010112.
                                                                                                                                                                                                                                                                                                                                                                                          complement(56244. .56319)
/rpt_family="Oryza sativa gene, repeat sequence Micropon-3
gil4586621|dbj|AB010113:1|AB010113"
complement(56244. .56317)
/rpt_family="Oryza sativa gene, repeat sequence Micropon-4
gi|4586620|dbj|AB010112.1|AB010112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSJN00196 113825 bp DNA linear HTG 17-JUL-2002 Oryza sativa chromosome 4 clone OSJNBb0020011, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
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Submitted (27-JUN-2002) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500* Cao Bao Road, Shanghai 200233,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DD 18148 GCCTTATARATTACTACCTCCATATTTTAATGTTTGACGCGGTGACTTTTCGTCCA 18089
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86.8%; Pred. No. 1.5e-22;
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                                                 /rpt_family="(TAA)n"
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                             /rpt_family="AT_rich" complement(50582..50
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Oryza sativa.
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ORGANISM

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Submitted (21-DEC-2001) Indian Initiative for Rice Genome Submitted (21-DEC-2001) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Delhi South Campus, New Delhi, Delhi 110021, India Research Program; Rennondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Rosearch Program; Rannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. Gaps between the contigs * are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes * of the gaps between them are based on estimates that have * provided by the submitter.
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1 (bases 1 to 158805)
Mohanty, A., *Basaki, T., *Matsumoto, T., *Yamamoto, K., Bharti, A.K., Raghuvanshi, S., Khurana, P., Khurana, J.P. and Tyagi, A.K.
Oryza sativa chromosome 11 PAC clone P0480H08, sequencing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propublished

( bases 1 to 158805)

Mohanty,A., #Sasaki,T., #Matsumoto,T., #Yamamoto,K., Bharti,A.K., Raghuvanshi,S., Khurana,P., Khurana,J.P. and Tyagi,A.K.

Direct Submission
90343 GATTCATCARABARGTCTTTAAGCATGACATAAATATTTTCATATTTGCACAAAATTT 90402
                                                                                                                                                                                                                                                   90403 TTAAATAAACGAATGGTTAAACGTTAGTCGAAAGTCAATGGCGTCATACATTAAAATA 90462
                                                                                                                                                                                                                    1006 --AAAAAAAGGAAFGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATA 1063
                                                                    951 GATTCGTCATCAAATATTTTTAAAGCATGACATAAACATTTTCATATTTGCAAAA----- 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC104847 11near HTG 21-DE Cryza sativa chromosome 11 clone P0480H08, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces.
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1 94637 94636 contig of 94636 bp in length 94637 136689; contig of 41935 bp in length 13690 136789; gap of unknown length 136790 140339; contig of 5550 bp in length 136790 140339; gap of unknown length 140390 140339; gap of unknown length
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/db_xref="taxon:4530"
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44993 a 34197 c 35594
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HTG; HTGS_PHASE2.
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AL Submission

AL Submission

Submitted (00-MAT-2002) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

On May 8, 2002 this sequence version replaced gi:18767489.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 9 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 10515: contig of 10515 bp in length

* 10616 23647: contig of 10515 bp in length

* 23548 36771: contig of 13024 bp in length

* 36872 44539: contig of 13024 bp in length

* 44440 44539: contig of 2668 bp in length

* 44440 44539: contig of 2602 bp in length

* 44640 72241: contig of 2002 bp in length

* 44640 72241: contig of 2002 bp in length

* 44640 72241: contig of 2002 bp in length

* 44640 72241: contig of 2002 bp in length
                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (19-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA (bases I to 164852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90223 CTTGTTAATATAATACCATCTCTATATTTTAATGTATGAACGCCGTTGACTTTTTGTCCAAC 90282
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86.6%; Pred. No. 5e-22;
tive 0; Mismatches 27; Indels 7;
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gap of unknown length
contig of 38988 bp in length
gap of unknown length
contig of 7039 bp in length
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150047: gap of unknown length
164852: contig of 14805 bp in length.
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/organism="Oryza sativa"
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/db_xref="taxon:4530"
/chromosome="3"
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2 (bases 1 to 164852)
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Best Local Similarity 86.6
Matches 220; Conservative
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                                  Oryza sativa.
Oryza sativa
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FEATURES

BASE COUNT

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87.2%;
                      Query Match
Best Local Similarity 87.28
Matches 218; Conservative
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Best Local
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Submitted (26-JUJ-2002) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr

- Web: www.genoscope.cns.fr)

On Jul 29, 2002 this sequence version replaced gi:19715885.

IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.

Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence any be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.

The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.

* NOTE: This sequence will be replaced

* This sequence will be replaced

* The finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSO7YPX
Oryza sativa chromosome 12 clone OJ1618_C05, *** SEQUENCING IN
PROGRESS ***, in ordered pieces.
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                                                                                                                                                                                                                                                                                                                       D 132432 AAATTICGAATAAAAGAATAGTCAAAGGTGGAGAAAGTCAAGGGCATCATACATTA 132491
                                                                                                 Db 132252 ATGTTAGTTTTAACTAATACTACCTCCATATTTTAATGTGCAACGCCGTTTACTTTTGT 132311
                                                                                                                                                             DD 132372 GACTIGATICGICATCGATGATCTTAAGCATGACATAAAAATATTTCATATTTGCACAA 132431
                                                                                                                                                                                                                                                                                                1006 A-----AAAAAAAGGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTA 1058
                                                                                                                                                                                                                     946 GACTIGALTICGICALGAATALTITITIAAGCAIGACATAAACAITITCALAITITGCAAAA 1005
                                                                                                                                      826 AIGGACCIATIACITALIACIACCICCATALITIAAIGIAIGACGCCGTICACTITIGT 885
                        Indels
    5.9e-22;
ches 31;
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/clone_lib="Monsanto"
46256 a 37378 c 36384 g 49645 t
    Pred. No. 5.9e
0; Mismatches
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/sub_species="japonica"
/db_xref="taxon:4530"
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Best Local Similarity 85.4%;
Matches 222; Conservative
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CNS07YPX
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Plant genes that confer resistance to strains of magnaporthe grisea
having av1 co39 cultivar specificity gene
Patent: WO 0234927.A 5 02-MAY-2002,
WISCONSIN ALUMNI RES FOUND (US); The Secretary of Agriculture (US)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                    19267 CTACTAGATAATACTATCTCCATATTTTAATGTATGACGCGGTTGACTTTTGTCCGAAGG 19326
                                                                                                                                                                                                                                                                                    Db 19447 IGPATRARARIGGECRARACGTTTGTCGRARAGTCAACGCATCATACATTAAAATAC 19506
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                                                                                                                                                                                                                                                    892 TITGACCATTCGTCTTATTAAAAAATTATGTATCTATTATTATTATTATGACTTG 951
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                                                                         Gaps
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                                                                      7;
Score 186, DB 2; Length 169663;
Pred. No. 6.9e-22;
0; Mismatches 25; Indels 7;
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/db_xraf="taxon:4530"
26676 a 19760 c 17854 g 27262 t
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HTG 13-MAY-2002

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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
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Khurana,J.P., #Linton,E.W., #Messing,J., Mohanty,A., Bharti,A.K., Raghuvanshi,S., Khurana,P. and Tyagi,A.K.

Cyraa sativa (apojea cultivar-group) chromosome 11 BAC clone
Ba0042J05, sequencing in progress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-MAY-2002) Indian Initiative for Rice Genome Sequencing, Department of Plant Molecular Biology, University of Dellhi South Campus, New Delhi, Delhi 110021, India # The Plant Genome Initiative at Rutgers - Waksman Institute, Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 154494)
Khurana.Jr., #Linton.E.W., #Messing.J., Mohanty,A., Bharti,A.K.
Rachuvanshi.S., Khurana.P. and Tyagi,A.K.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
# The Plant Genome Initiative at Rutgers - Waksman Institute,
Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group) chromosome 11 clone
Ba0042J05, *** SEQUENCING IN PROGRESS ***, 7 ordered pieces
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Location/Qualifiers
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/db_xref="taxon:39947"
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Pred, No. 9.4e-22;
                                                                                                                                                                                     DNA
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                                               Db 103483 GAGGGAGTATGTTTTTCAATGCATTA 103457
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                     GAGGGATTATATGGGATAGCTACAGTA 1092
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44561 a 32837 c 31980 q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Submitted (30-JAN-2002) Takuji Sasaki, National Institute of Agrobiogical Sciences, Rice Genome Research Program; Kannondai 2-1-2, Taukuba, Ibaraki 305-8802, Japan (E-mail:tsasaki@idas affcc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                      AP004691 148441 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone P0453D01, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group)
Bukaryochyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                             Oryza satira (japonica cultivar-group) (cultivar:Nippombare) DNA,
clone:P0453D01.
33651 ACAAAATTTTGAATAAAACGAATGGTCAAATGTTGATCGAAAAGTCAAAAGGCGTCATAC 33592
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
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the accossion number will be preserved.
Location/Qualifiers
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
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Pred. No. 8.6e-22;
0; Mismatches 36;
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2 (bases 1 to 148441)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
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31475 c 33016 g 41500 t
                                                                     /chromosome="8"
                                           1055 ATTAAAATACGGAGGGATTA 1074
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Best Local Similarity 83.9%;
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NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.
                                                                                  DD 144949 GATGATAGGCAAGTGAAGCACGTGCTTTATTTTATTACTACCTCCGTATTTTAATGCAT 145008
                                                                                                                                                                               Db 145069 TTATCATTTATTATTATGACTTGATTTGTTATCAAATGTTCTTTAAGCATGACATAAA 145128
                                                                                                                                                                                                                                                                                                                                                                                       DD 145129 TATTICATATTIGCACAAAATTITTGAATAAAACGAATGGTCAAACATIGGTCGAAAAG 145188
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Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0024C06.
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                                                     807 GTTGCAACGGAATAGTAATATGGACCTATTACTTACTACTACTCCTCCATATTTTAATGTAT 866
                                                                                                                                                  GACGCCGTTCACTTTTTGTCCAACGTTTGACCATTCGTCTTATAAAAAATTATGTAT 926
     Gaps
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Direct Submission
Submitted (29-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC
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the accession number will be preserved.
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23082 23186: gap of 105 bp
23187 179486: contig of 156300 bp in length.
Location/Qualifiers
     Indels
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23081 23081: contig of 1 bp in length
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     43;
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  0; Mismatches
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2 (bases 1 to 179486)
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/organism="Oryza sativa (japonica cultivar-group)"

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Pred. No. 1.2e-21;
0; Mismatches 29;
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                                                                             50872 a 39291 c 39711 g 49023
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
                                                         /clone="P0024C06"
                                                                                                                                   Query Match 8.4%;
Best Local Similarity 85.9%;
Matches 219; Conservative
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(without alignments)
14774.266 Million cell updates/sec
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1 cgtcgttcgttttgtgcatc.....tagcttgtgctttgctgta 2201
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	BAC clone K6P36 fr	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Rice lipoxydenase	Arabidopsis thalia	Sakuranetin syntha	Oryza sativa MLO q	Oryza sativa gcpE
SUMMARIES	ID	AAD38803	AAC52171	ABQ85736	AAC47067	ABK15663	ABQ65731	AAA99467	AAV35027	AAD31202
	DB	24	21	24	21	24	24	21	13	24
	Query Match Length DB	91552	807	356	1126	4569	689	5241	7175	33675
ф	Query	8.4	5.7	5.7	5.7	5.1	5.0	4.8	4.6	4.5
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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16-APR-1999;
16-APR-1999;
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21-JUN-1999;
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23-APR-1
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      The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and 861094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The Pi-CO39(1) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-CO39(1) nucleic acids may be used as probes to detect the presence of pure Pi-CO39(1) proteins. Purified gene products of Pi-CO39(1) proteins. Purified gene products of Pi-CO39(1) are useful in producing polyclonal or monoclonal artibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(1) compared to the presence and accumulation of Pi-CO39(1) compared in products of plants are useful for plant breeding or directly in agricultural or horitoultural applications. The present sequence is BAC clone K6936 from rice variety CO39.
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New PiCO39(t) polynucleotides from chromosome 11 of indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
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                                                                                                   Example 2; Page 68-110; 175pp; English.
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1334 AAGATTTGCAGGTGCGAGATCACTCTTTCACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
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                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                       5.7%; Score 125.2; DB 21; Length 807; 65.9%; Pred. No. 1.5e-17; tive 2; Mismatches 90; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCAGGAAGATCAAGGAGAAGGACCGAC 1483
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990S-0155596.
990S-0157753.
990S-0157753.
990S-0158029.
990S-0158029.
990S-0158029.
990S-0159293.
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990S-0160981.
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ID ABQ85736 standard; DNA; 356
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                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 178; Conserv
28-SEP-1999)
29-SEP-1999)
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22-0CT-1999;
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26-0CT-1999;
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26-0CT-1999;
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Arabidopsis thaliana expressed polynucleotide SEQ ID NO 606 Plant; Arabidopsis; transgenic; fungicide; insecticide; ds.

23-MAY-2002

(HAMI/) (PRIC/)

RAIN/) YUYY/)

(GORL/)

(RAME/) (PAGE/) (MATH/) (LEDF/)

(WOES/) (HAAS/) (GARC/)

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1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGAAG 1453
                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 52441.
                                                                                              1454 CICAGGAAGAICAAGGAGAAGGAGACCGAC 1483
                                                                                                                       44 CTGAGGAAGATCAAGGAGAAGGACTCAGAC 15
                                                                                                                                                                                                                                                           AAC47067 standard; DNA; 1126 BP.
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990S-0131449
990S-0132407
990S-0132407
990S-0132485
990S-0132485
990S-0132485
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990S-0134218.
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99US-0135629.
99US-0136021.
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99US-0136782.
99US-0137222.
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99US-0137724.
99US-0138094.
99US-0138540.
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99US-0123180.
99US-0123548.
99US-0125788.
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99US-0127462
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                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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25-MAY-1999;
27-MAY-1999;
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25-WAR-1999
29-WAR-1999)
01-APR-1999)
06-APR-1999)
116-APR-1999
21-APR-1999
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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14-MAY-1999;
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09-MAR-1999)
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30-APR-1
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23-APR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid of Arabidopsis thaliana comperising a sequence capable of hybridising under stringency to one of the 999 sequences referred to but not defined in the specification (ABQ85131-ABQ86129). The nucleic acid sequences are useful to identify homologous or related genes, to produce compositions that modulate expression or function of the encoded protein, to map functional regions of the protein, to study associated physiological pathways, to genetically manipulate cells and plants. The encoded products are useful to screen for biologically active agents such as fungicides or insecticides and to elucidate biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1334 AAGATTTGCAGGTGCGAGATCACTCTTTCACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences of Arabidopsis thaliana and their encoded products are useful to produce transgenic plants, to screen for biologically active agents such as fungicides and insecticides and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 CTTGTGAGAGAAGTTGATGTAAGACTCTCTGTTCGTGGTGGAGAGTTTGGTAAAGGCCCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Price JL, Raines TM, Yu Y;
Ledford BL, Woessner JP, Haas WD;
Davis KR, Allen K, Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 606; 18pp + Sequence Listing; English.
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A, Mathew AV, L4
r M, Slater T, 1
                                                                                                                                         26-JAN-2001; 2001US-0770791.
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Page A, Ma
Kricker M,
                                                                                                                                                                                                                                                              AN Y.
HAMILTON C M.
PRICE J L.
RAINES T M.
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MATHEW A V.
LEDFORD B L.
WOESSNER J P.
    Arabidopsis thaliana.
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GARCIA C A.
KRICKER M.
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DAVIS K R.
ALLEN K.
HOFFMAN N.
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                                                                                                                                                                                                                                       GORLACH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genetic studies
                                                 US2002062014-A1.
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Rameaka JG,
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Garcia CA, Hurban P;

(KRIC/) (SLAT/) (DAVI/) (ALLE/) (HOFF/)

Query Match

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90S-0138847 90S-0139119 90S-0139419 90S-0139429 90S-0139429 90S-0139459 90S-0139459 90S-0139459 90S-0139459 90S-0139459 90S-0139459 90S-0139459 90S-0139459 90S-0139763	990'S 01408554 990'S 01408554 990'S 0140891. 990'S 0141842 990'S 0142154 990'S 0142154 990'S 0142390 990'S 0142390 990'S 0142390 990'S 0142390 990'S 0142390 990'S 014332 990'S 0144332 990'S 0144333 990'S 0144333	905-0145088 905-0145088 905-0145089 905-0145089 905-0145185 905-0145185 905-0145218 905-0145218 905-0145218 905-0145218 905-0145218 905-0145218 905-014720 905-014720 905-014720 905-014720 905-014720 905-014720 905-014720 905-014720 905-014720 905-014720
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90S - 014817 90S - 014831 90S - 014834 90S - 014856 90S - 014936 90S - 014972 90S - 014972 90S - 014972 90S - 014993	905-012089 905-012108 905-015108 905-015108 905-015108 905-0151308 905-0151307 905-015307 905-015407 905-015407 905-015407 905-015407 905-015565	9995-0157117 9995-015713 9995-015763 9995-0158029 9995-0158029 9905-015829 9905-015929 9905-015929 9905-015931 9905-015931 9905-015931 9905-015931 9905-015964 9905-015967 9905-016077 9905-016076	005-016098 005-016098 005-016098 005-016140 005-016140 005-016136 005-016136 005-016136 005-016136 005-016136 005-016136 005-016136 005-016136 005-016136
0-AUG-1999 22-AUG-1999 32-AUG-1999 33-AUG-1999 6-AUG-1999 6-AUG-1999 0-AUG-1999 0-AUG-1999 0-AUG-1999 33-AUG-1999 5-AUG-1999	7. Aug. 1999 7. Aug. 1999 7. Aug. 1999 7. Aug. 1999 7. Aug. 1999 7. SEP 1999 6. SEP 1999 6. SEP 1999 7. SEP 1999 7. SEP 1999 7. SEP 1999 7. SEP 1999	04-00CT-1999; 06-00CT-1999; 07-00CT-1999; 08-00CT-1999; 12-00CT-1999; 13-00CT-1999; 13-00CT-1999; 14-00CT-1999; 14-00CT-1999; 14-00CT-1999; 14-00CT-1999; 121-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999; 21-00CT-1999;	2.007-199 2.007-199 2.007-199 2.007-199 3.007-199 3.007-199 3.007-199 3.007-199 3.007-199
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QY 1214 GACAAGGTGAAGGACACATCGAGGAGAAGGCGGGGAAGCAGTGGCGAAGCACAGG 1273

Query Match 5.7%; Score 124.4; DB 21; Length 1126; Best Local Similarity 66.3%; Pred. No. 2.6e-17; Matches 179; Conservative 0; Mismatches 91; Indels 0;

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US2002059663-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inducible expression of an associated nucleotide sequence. Also
included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone
for the lipoxygenase gene, promoter fragments, the lipoxygenase transit
peptide which directs expressed proteins to the plastid, a vector
comprising the promoter or fragments and a transgenic plant comprising
the vector. The promoter or fragments are useful for expressing a
nucleotide sequence of interest. The transit peptide is useful for
targeting an associated protein of interest to plastids. A nucleic acid
which expresses polypeptide having lipoxygenase activity is useful for
inhibiting fungal mycotoxins when transformed into a plant. The
lipoxygenase is useful for inhibiting fungal mycotoxins. The promoter is
useful for regulating transcription of a chemically inducible but not
wound or pathogen inducible gene, which involves applying a chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ōţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid molecule (a promoter rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving chemically-inducible but not wound or pathogen-
                                                                           1393
                                                                                                                           1453
                         1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCCGCGCGTGGCGAGCTCAGCCCAAGGTCCC 1333
                                                                                                   560
                                                                                                                                                    561 GAAGATGCTGAGACAGTATACGCTTGTATCGACTTGGTATCAACGATAATACAGAGGAAG 620
381 GAGCCAATTAAGCAGCATGTTGAAGAGAAAGTAGGCAAATCTGTTCAGAAACACAGTCAT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound or pathogen-inducible expression of an associated nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                       Rice; ds; lipoxygenase; RCI-1; transgenic; plant; plant antifungal; rice chemically induced cDNA; promoter; transit peptide; plastid; fungal mycotoxin inhibitor; plant breeding; pBSK+LOX4a.
                                         1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGGAAG
                                                                                                                                                                             1454 CTCAGGAAGATCAAGGAGAAGGAGACCGAC 1483
                                                                                                                                                                                                    621 CTGAGGAGGACAGGACTCAGAC 650
                                                                                                                                                                                                                                                                                                                                               Rice lipoxygenase gene 4.5kb fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 68-69; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000GB-0022739
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schaffrath,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYZU-) UNIV ZUERICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-188550/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200206490-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                                     21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dudler R,
                                                                                                                                                                                                                                                                                              ABK15663;
                                                                                                                                                                                                                                                                                                                                                                        Rice;
                                                                                                                                                                                                                                           RESULT 5
ABK15663
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                                                                                                                          δŏ
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                                                                                                                                                                             Qγ
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regulator to a plant or seed containing a chemically regulatable nucleotide sequence. Transgenic plants as described above are useful for breeding improved plant lines that for example increases the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to their petinised genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence is the 4.5kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana, thale cress, plant; transgenic; GMO; disease; stress; metabolic pathway; biosynthetic pathway; nutrition; fungicide; insecticide; antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2963 AIAGTACTITAAGTGTGATTTATATTTTTACATAAAATTTTTGAATAAGACGA 3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2845 IACTACCICTGTTTTTTAATAGATGACGCCGTTGACTTTTTTCTCACATGTTTGACCATTC 2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3023 ATGGTCAAACATGGGAGAAAAGTCAACGGCGTCATCTATTAAAAACGGAGAGAGTATA 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843 IACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCACGTTTGACCATTC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         903 GICTIBITARARARAPITATGTATCTATTATTATTATTATTATGACTTGATTCGTCATCA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2905 GICTTATT - AAAAATTATATATATATTATAATTTAGTTTGTTATGAATTGTTTTATCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963 AATAITITITAAGCATGACATAAACATTTTCATATTTGCAAAAA------AAAAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 ATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 111.2; DB 24; Length 4569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4569 BP; 1234 A; 1051 C; 980 G; 1304 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                 fragment of the RCI-1 gene from plasmid pBSK+LOX4a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana polynucleotide SEQ ID NO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1077 IGGGATACCTACAGTAGCAGAGTCATGATAAA 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3083 TGATTCATCGGAATTAAAAATAGACGGTATA 3114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABQ657.31 standard; DNA; 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-2000; 2000US-178506P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.1
Best Local Similarity 68.4
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AN Y.
HAMILTON C M.
PRICE J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEDFORD B L. WOESSNER J P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAINES T M.
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Sakuranetin synthetase gene encoding protein with naringenin 7-0-methyltransferase activity in rice cells and promoter activity, used to derive sakuranetin from naringenin easily in plants to impart
                                                                                                                                                       SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                         Claim 1; Page 43-46; 57pp; Japanese
     transgenic plant;
                                                                                                                                                                                                                                                                                 antibacterial characteristics
                                                                                                    03-MAR-2000; 2000WO-JP01306
                                                                                                                              99JP-0057748
                                                                                                                                                                                                        WPI; 2000-572186/53.
                                                                                                                                                                                                                    P-PSDB; AAB26843.
     intibacterial;
                                                   WO200052174-Al
                                                                                                                                                       (NISC-) JAPAN
                              Oryza sativa
                                                                                                                               04-MAR-1999;
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                                                                              08-SEP-2000,
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                                                                                                                                                                                Kodama 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                              The invention relates to nucleic acids (1) that hybridise under stringent conditions to any of 999 sequences (ABQ6444-ABQ6642) or their fragments. (1) are used to express the corresponding polypeptides (II) or to produce genetically modified plant cells or transgenic plants, which may have improved resistance to disease or stress, or altered metabolic/blosynthetic pathways (for production of commercial, nutritional or medicinal products), or generally any trait of interest, or can be used to screen for biologically active agents (e.g. fungicides, insecticides and antibiotics).
                                                                                                                                                                                                                                                                                                                                                                                            printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1214 GAGAAGGTGAAGGAGCACATCGAGGAGAAAGGCGGGAGAGCAGTGGCGAAGCACAGCCAG 1273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCCGCGGTGGCGAGCTCAGCCGAGCTCCC 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1334 AAGATTTGCAGGTGCGAGATCACTCTTTTACCAAGCGCCACGGCGTCATCCGCGCCGAG 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1394 GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGGAAG 1453
                                                                                                                                                                                                New nucleic acid that hybridizes to Arabidopsis thaliana sequences, useful e.g. for preparing transgenic plants with increased resistance or altered metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 GAGCCAATTAAGCAGCATGTTGAAGAGAAAGTAGGCAAATCTGTTCAGAAACACAGTCAT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø.
                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the pr
specification, but was obtained in electronic format directly from
USPTO at seqdata.uspto.gov/sequence.html?DocID=999909770149.
                                                                                                                  Yu Y;
JP, Haas W
Hoffman N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakuranetin synthetase; naringenin 7-0-methyltransferase; NOMT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.0%; Score 110.2; DB 24; Length 689; 62.2%; Pred. No. 2.7e-14;
Live 0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 308; 40pp + Sequence Listing; English.
                                                                                                                  Price JL, Raines TM,
Ledford BL, Woessner
Davis KR, Allen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 689 BP; 192 A; 136 C; 174 G; 176 T; 11 other;
                                                                                                                1454 CTCAGGAAGATCAAGGAGAAGG 1475
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                                                                                                                              Page A, N
Kricker M,
HAAS W D.
GARCIA C A.
KRICKER M.
                                                                                                                                                                             WPI; 2002-479224/51.
                                       SLATER T.
DAVIS K R.
ALLEN K.
HOFFMAN N.
HURBAN P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                  An Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-2001
                                                                                                                            Rameaka JG,
                                                                                                                                          Garcia CA,
Hurban P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163;
                                                                                                                   Gorlach J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA99467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                   (DAVI/)
(ALLE/)
(HOFF/)
                           (KRIC/)
(SLAT/)
                                                                                          (HURB/)
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Matches
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This invention relates to a sakuranetin synthetase gene encoding a protein with naringenin 7-0-methyltransferase (NOMT) sctivity and promoter activity. The invention includes a recombinant vector including the sakuranetin synthetase DNA and host cells transformed with the vector. The sakuranetin synthetase protein has antibacterial activity and is used to produce transpenic plants with antibacterial characteristics. The present sequence represents the sakuranetin synthetase gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                960 TCAAATATTTTTAAGCATGACATAAACATTTTTCATATTTGCAAAA-----AAAAAAA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1013 ACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATAACATTAAAATACGGAGGGAT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4905 ITABARATATATACTITCATGTACACATATAATTITTACTTATTTCATAAATTTTTTTGAATAAAG 4964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840 TATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCA 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              900 TICGICITALIAAAAAATTATGIAICIATTATITATITATITATTATGACTIGATICGICA 959
                                                                                                                                                                                                                                                                                                                                                                                               Length 5241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATATGGGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTT 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATGTAGTAGTAGTAGTAAAAATACTACATGATATGATGGTATGTT 5073
                                                                                                                                                                                                                                                                                                                            Sequence 5241 BP; 1542 A; 1138 C; 1094 G; 1467 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            4.8%; Score 106.6; DB 21; 63.3%; Pred. No. 4e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4e-13;
); Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barley; MLO; mildew; pathogen; resistance; ss.
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Matches 183; Conser
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*tag= c note= "This region corresponds to rice GCPE protein \sharp 1"
                                                                                                                                                         /*tag= d
//tote="This region corresponds to rice GCPE protein #1"
//cons.splice= (5'site:YES, 3'site:NO)
6924..7019
                                                        "Rice GCPE protein #1"
                                                                                             "Rice GCPE protein #2"
                      Location/Qualifiers
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10294..10693
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10694..10798
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.0134..10293
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6924. 11129
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9589..9730
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8154..8252
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8253..8369
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8370..8514
/*tag= r
8515..8589
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8590..9011
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9072..9162
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9163..9225
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9328..9472
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9473..9588
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1731..9950
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9012..9071
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3226..9327
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6514..6762
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7020..7162
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7163..7269
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7814..7922
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7923..8153
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7270..7343
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7344..7444
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7445..7524
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Oryza sativa.
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                       Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gcpE gene; methyl-D-erythritol phosphate; MEP; dimethylallyl diphosphate; transgenic plant; isoprenoid compound; tocopherol; isopentyl diphosphate; food; feed source; transfection; single nucleotide polymorphism; SNP; oxidative stress tolerance; U tolerance; transformation; rice; plant;
                                                                                                                                                                                                                                                                                              The sequence is that of the MLO gene, wild-type Mlo exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of Mlo function may be used to stimulate a defence response in transgenic plants conferring increased pathogen resistance, especially resistance to powdery mildew or rust. The product can also hee used for identifying compounds able to stimulate a defence response in a plant by interaction with encoded polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1911 CCTCCAPCTCTAAATATTTTGACGCGGTTGACTTTTTTTAAATATGTTTGACCATTCGTCTT 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             968 ITITIAAGCATGACATAAACATTITCATATTIGCAAAA-----AAAAAAAAAAAGG 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2031 ACTATTATGTATACCATATAGFTTTTACATATTTCACTAAAGTTTTTTAAATAAGACGAATGG 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                908 ATTAAAAAAAATTATGTATCTATTATTTATTTTATTATGACTTGATTCGTCATCAAAAA 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 CCICCATAITITAAIGTAIGACGCCGTICACTITITGTCCAACGITTGACCATICGTCTT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATAT 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Mlo gene of barley - used to develop products for the production of transgenic plants which have increased pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                4.6%; Score 101; DB 19; Length 7175; 67.5%; Pred. No. 7.8e-12; tive 0; Mismatches 70; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7175 BP; 2089 A; 1455 C; 1431 G; 2200 T; 0 other;
                                                                                                                                                                              Bueschges R, Panstruga R, Schulzelefert PMJ;
                                                                                                                                                        CENT INNOVATIONS LTD JOHN.
                                                                                                                                                                                                                                                                          Disclosure; Fig 8; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD31202 standard; DNA; 33675 BP.
                                                                                 97WO-GB02046.
                                                                                                         97GB-0004789.
                                                                                                                   96GB-0015879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa gcpE gene.
                                                                                                                                                                                                      WPI; 1998-159149/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                         (INNE-) INNES
                                                                                                        07-MAR-1997;
29-JUL-1996;
30-OCT-1996;
             Oryza sativa
                                                                                   29-JUL-1997;
                                    WO9804586-A2
                                                            05-FEB-1998
                                                                                                                                                                                                                                                      resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD31202;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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QYg δ AAD38804 standard; DNA; 69300 BP

AAD38804/c

RESULT 10

(first entry)

23-SEP-2002

AAD38804;

16578 ATCCTGTATCTATCGT 16563

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The invention relates to gcpE nucleic acid molecule, an essential gene of methyl-D-erythritol phosphate (MEP) pathway) that encodes rice, Arabidopsis thallana or Escherichia coll GCPE protein. gcpE is useful for producing a transgenic plant such as Brassica campestris, B. napus, canola, castor bean, coconut, cotton, crambe, linseed, maize, mustard, oil palm, peanut, rapessed, rice, safilower, seasane, soybean, sunflower, or wheat with an increased isopremoid (tocopherol) compound level. The expression of GCPE protein in organisms increases the level of tocopherol substrate such as isopermy diphosphate and dimethylallyl diphosphate bhosynthesis. Transgenic organisms overexpressing GCPE protein in transgenic organisms overexpressing GCPE protein in transgenic plant may provide tolerance to stresses e.g., oxidative stress tolerance such as to oxygen or ozone, UV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the same species, and to obtain nucleic acid homologues. gopf is also used as or primers. The recombinant vectors are used in plant transformation or transfection. gopf an also act as markers capable of detecting polymorphisms such as single nucleotide polymorphisms (SNFS). gopE is also used to determine the level or pattern of expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16698 AATATACTTTTATGTATACATATAGTTTTATATTTTCACAAAATTTTTGAATAAGATG 16639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gops nucleic acid which is an essential gene of the methyl-D-erythritol phosphate pathway, encoding a fully defined GCPE protein which is useful for increasing levels of tocopherol substrates in plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16757 GTCTTATICAAAAATTIAAATAAGTATTATTT-TTTTCCTATCATTGATTCATTGTTA 16699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1016 AATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTAT 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843 TACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTC 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seeman M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33675 BP; 9475 A; 7073 C; 7297 G; 9801 T; 29 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein. The present sequence is Oryza sativa gcpE gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez-concepcion M, Rohmer M, 1 TV, Venkatramesh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Page 97-117; 155pp; English
/*tag= ag
10799..11027
/*tag= ah
11028..11129
/*tag= ai
                                                                                                                                                                                                                                                                                                                                                                                                             07-AUG-2000; 2000US-223483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MONS ) MONSANTO TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campos N, Rodri
Venkatesh TV,
                                                                                                                                                                                                                                                                                                                                         06-AUG-2001; 2001WO-US24335
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P-PSDB; AAE19651, AAE19652.
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ses 173; Conserv
                                                                                                                                                                                                        WO200212478-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boronat A, Car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-CO39. The P1-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The P1-CO39(t) nucleic acids may be used as probes to detect the presence of p1-CO39(t) nucleic acids may be used as probes to detect the presence of our P1-CO39(t) proteins. Purified gene products of P1-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of P1-CO39(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or hortcultural apphications. The present sequence is BAC clone E2P5 from rice variety CO39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65529 cercegreceraararrigaegecerraacririraaararargrigaregriegrer 65470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New PiCO39(t) polynucleotides from chromosome 11 of Indica rice utilivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-CO39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTAAAAAAAATTATGTATCTATTATTTATTTATGACTTGATTCGTCATCAAATAT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCICCAIATITIAAIGIAIGACGCCGIICACIITITIGICCAACGIIIGACCAIICGICII 907
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                                                                                                                                             Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene;
AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding;
resistance; agricultural; horticultural; plant protectant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 100; DB 24;
Pred. No. 3.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Durfee TJ;
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                                                                                                           BAC clone E2P5 from rice variety CO39.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chauhan RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           USDA ) US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.4%;
                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2001; 2001US-303897P.
                                                                                                                                                                                                                                                                                                                                                                                20-0CT-2000; 2000US-242313P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SA, Farman ML,
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                                                                                                                                                                                                                                                                   WO200234927-A2.
                                                                                                                                                                                                                              Oryza sativa.
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1021 TCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATA 1076
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Rice; ds; lipoxygenase; RCI-1; transgenic; plant; plant antifungal; rice chemically induced cDNA; promoter; transit peptide; plastid; fungal mycotoxin inhibitor; plant breeding; pBSK+LOX4a. Rice lipoxygenase gene 4.5kb fragment. ABK15663 standard; DNA; 4569 BP. (first entry) Oryza sativa. 21-MAY-2002 ABK15663; RESULT 11

(SYGN ) SYNGENTA PARTICIPATIONS AG. (UYZU-) UNIV ZUERICH. Lawton KA; .2-JUL-2001; 2001WO-EP08085 13-JUL-2000; 2000GB-0017275 15-SEP-2000; 2000GB-0022739 Schaffrath, WPI; 2002-188550/24. WO200206490-A1. 24-JAN-2002. Dudler R,

Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound or pathogen-inducible expression of an associated nucleotide sequence Claim 3; Page 68-69; 88pp; English.

the vector. The promoter of fragments are useful for expressing a nucleotide sequence of interest. The transit peptide is useful for targeting an associated protein of interest to plastids. A nucleic acid which expresses polypeptide having lipoxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. The promoter is useful for requiating transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical regulator to a plant or seed containing a chemically inducible but not nucleotide sequence. Transgenic plants as described above are useful for breeding improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. New crops with improved stress tolerance can be obtained that, due to invention relates to an isolated nucleic acid molecule (a promoter of rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) expable of driving chemically-inducible but not wound or pathogen-inducible expression of an associated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector comprising the promoter or fragments and a transgenic plant comprising their optimised genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence is the 4.5kb fragment of the RCI-1 gene from plasmid pBSK+LOX4a. 

Sequence 4569 BP; 1234 A; 1051 C; 980 G; 1304 T; 0 other;

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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene AVR1-C039. The Pi-C039(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-C039(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-C039(t) genes, and to produce large quantities of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
                                                                                                                                                                                                                                                                                    1078
                                                                                                                                                                                                                                                                                                         3021
                                                                                                                                           962.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants
                                     Gaps
                                                                                              3080 TACTCTCTGTTTTTTAATAGATGACGCCGTTGACTTTTTCTCCCATGTTTGACATTTC
                                                                      843 TACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTC
                                                                                                                                           903 GICTTATTAAAAAATTATGTATCTATTATTATTTATTATTATGACTTGATTCGTCATCA
                                                                                                                                                                              3020 GICTTATICAAAAITTTATGTAAAIGTATAAGATATAAATCACACTTAAAGTACTATGA
                                                                                                                                                                                                                                                 2960 GIGATAAAACAATICATAACAAACTAAATTATAATTATAATTITTTAATAAAAAT
                                                                                                                                                                                                                                                                                    1019 GGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTATATG
                                                                                                                                                                                                                  963 AATATTTTTAAGCAIGACATAAACATTTTCATATTTGCAAA----AAAAAAAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rice, chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of to strains of Magnaporthe grisea or other plant pathogens with avitulence gene AVR1-CO39
                                     4.
Length 4569;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                            2840 TTATATACAATCTAATTATGGTAAGCAAAAATATTT 2798
                                                                                                                                                                                                                                                                                                                                                         1079 GGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTT 1121
Score 98.6; DB 24;
Pred. No. 2.1e-11;
                                   0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Durfee IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BAC clone K6P36 from rice variety C039
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(USDA ) US DEPT OF AGRICULTURE.
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4.5%;
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09-JUL-2001; 2001US-303897P.
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                                     Conservative
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                    Similarity
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                    Best Local Sim.
Matches 175;
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   Query Match
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99US-0138840
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     pure Pi-C039(t) proteins. Purified gene products of Pi-C039(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-C039(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or hortkoultural applications. The present sequence is BAC clone K6P36 from rice variety C039.
                                                                                                                                                                             33565 TAGTAAGTACTCCCTCCGTATTITAACGTAIGACGCCGTTGACTTTTCGATCAACATTTG 33624
                                                                                                                                                                                                                       1009 AAAAACGAATGGICAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAG 1058
                                                                                                                                                                                                         956 GTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAAA-----AA 1008
                                                                                                                              836 TACTIALTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTTGTCCAACGTTTG 895
                                                                                                                                                                    7; Gaps
                                                                                       4.5%; Score 98.2; DB 24; Length 91552; 65.6%; Pred. No. 9.8e-11; tive 0; Mismatches 78; Indels 7;
                                                                    Sequence 91552 BP; 26676 A; 19760 C; 17854 G; 27262 T; 0 other;
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990S-0128714.
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99US-0123180.
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99US-0126264.
99US-0126785.
99US-0127462.
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99US-0132048
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Matches 162; Conservative
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                                     22-JUL-1999;
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1693 TGTGAATGCAGGTGCTGCACCAAGGTGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGG 1752
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                                                                                                                                                                                                                                                                                                                                                    Query Match 4.3%; Score 95.4; DB 21; Length 694; Best Local Similarity 67.2%; Pred. No. 4.6e-11; Matches 135; Conservative 0; Mismatches 66; Indels 0
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99US-0160768
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990S-0144632. 990S-0144884. 990S-0144814. 990S-0145086. 990S-0145085. 990S-0145087. 990S-0145087.	9905-0145218 9905-0145218 9905-0145218 9905-0145913 9905-0145913 9905-0145511 9905-0145512 9905-0146386 9905-0146386 9905-0147038 9905-0147038	990S - 0147260 990S - 0147303 990S - 0147493 990S - 0147493 990S - 0148319 990S - 0148310 990S - 0148341 990S - 0148365 990S - 014836 990S - 0149368 990S - 014973 990S - 0149723 990S - 0149723	99US-0149930. 99US-0150866. 99US-0151085. 99US-0151066. 99US-0151080. 99US-0151303. 99US-0151303. 99US-0151333. 99US-0151333. 99US-0151333.	990S-0155130. 990S-0155539. 990S-0155458. 990S-0156458. 990S-0156396. 990S-0157717. 990S-015836. 990S-015836. 990S-0159294. 990S-0159295.
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99US-0130810. 99US-0130891. 99US-0131449. 99US-0132048. 99US-0132484. 99US-0132485. 99US-0132486. 99US-0132486.	9905-0134216. 9905-0134218. 9905-0134211. 9905-0134770. 9905-0134770. 9905-0134778. 9905-0135124. 9905-013523. 9905-0135629. 9905-0135629.	99US-0137528. 99US-0137524. 99US-013754. 99US-0138094. 99US-0138119. 99US-0139452. 99US-0139452. 99US-0139455. 99US-0139455. 99US-0139456. 99US-0139456.	9905-0139461. 9905-0139462. 9905-0139463. 9905-0139750. 9905-0139817. 9905-0140899. 9905-0140899. 9905-0140895. 9905-0140897. 9905-0141287.	9905-0142055. 9905-0142390. 9905-0142920. 9905-01429477. 9905-0144042. 9905-0144085. 9905-0144085. 9905-0144335. 9905-0144333. 9905-0144333. 9905-0144333.
23-APR-1999; 23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999; 04-MAY-1999; 06-MAY-1999; 06-MAY-1999; 06-MAY-1999;	11 - MAY 1999; 14 - MAY 1999; 14 - MAY 1999; 18 - MAY 1999; 19 - MAY 1999; 20 - MAY 1999; 21 - MAY 1999; 25 - MAY 1999; 25 - MAY 1999; 27 - MAY 1999; 27 - MAY 1999; 28 - MAY 1999; 28 - MAY 1999;	03 - JUN-1999; 04 - JUN-1999; 08 - JUN-1999; 10 - JUN-1999; 14 - JUN-1999; 14 - JUN-1999; 16 - JUN-1999; 18 - JUN-1999;	18-JUN-1999) 18-JUN-1999) 18-JUN-1999) 18-JUN-1999) 21-JUN-1999) 23-JUN-1999) 23-JUN-1999) 29-JUN-1999) 30-JUN-1999) 30-JUN-1999) 30-JUN-1999) 30-JUN-1999)	02-JUL-1999; 08-JUL-1999; 08-JUL-1999; 12-JUL-1999; 13-JUL-1999; 14-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;
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                                                                                                                                                                                                                                                            1693 IGTGAATGCAGGTGGTGCGCACCAAGGTGTTCGAGATGCCGCCGCTGTCGGTGGAGGAGG 1752
                                                                                                                                                                                                                                                                                                  1753 CGATGGAGCAGCTAGTGAATGTGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACCG 1812
                                                                                                                                                                                                                                                                                                                                        240 TGATCAAGGAGATTGTCCGTACCAAGACTTTCGAGATGCCACCATTGACTGTCGCGTGAGG 299
                                                                                                                                                                                                                                                                                                              300 CAGTCGAGCAGCTGGAACTAGTCAGTCACGACTTCTATGGCTTCCAAAATGAAAAACTG 359
                                                                                                                                                                                                                                                                                                                                                           360 GTGAGATAAACATAGTGTACAAGAGAAAAGAAGGAGGTTACGGTCTGATAATCCCAAAGA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pathogen inducible regulatory element; MAG-7; Magnaporthe grisea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa pathogen inducible regulatory element Pr-10c cDNA
                                                                                                                                                                                                                       Length 695;
                                                                                                                                                                                                                      4.3%; Score 95.4; DB 21;
67.2%; Pred. No. 4.6e-11;
tive 0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                              1873 GAGACGGTCATCTCCACAAGG 1893
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                                                                                                                       99US-0161405.
99US-0161406.
99US-0161359.
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                                                                                            99US-0160981,
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99US-0161361
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99US-0161992
                  99US-0159584
                                             99US-0160768
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                                                                                    99US-0160980
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Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-511872/47.
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                                                                                                                                                                                28-0CT-1999;
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                                             21-0CT-1999;
                                                       21-OCT-1999;
                                                                 21-0CT-1999
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                                                                         1-0CT-1
2-0CT-1
                                                                                                                       25-0CT-1
25-0CT-1
26-0CT-1
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                                                                                                                                                              26-0CT-
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                                                                                                                                                            The present sequence, Pr-10c, is a pathogen inducible regulatory element. It was identified by screening a Co39 rice seedling aconic cos9 library with a cDNa clone, MAG-7 of a gene whose transcripts appeared in cos9 rice seedlings 72 hours after incoulation with Magnaporthe grisea. Induced expression of the Pr-10c gene was not detected after infection with M. grisea throughout a 144 hour time period. The Pr-10c sequence is used to make a novel plant expression vector comprising a pathogen-inducible regulatory element and a core promoter, where the regulatory element is selected from three rice genomic DNA sequences AMI93778-80. The vectors are used for increasing the disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  958 CATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTGCAAAA-----AAAAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 ATTACTACCICCATATTTTAATGTATGACGCCGTICACTTTTTGT---CCAACGTTTGAC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 898 CATTCGICTTAITAAAAAAAATTAIGTATCTATTATTITATTATGACTTGATTCGT 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant expression vector with pathogen-inducible regulatory element used for increasing disease resistance of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 91.4; DB 18; Length 1591;
Pred. No. 5e-10;
0; Mismatches 71; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1591 BP; 464 A; 289 C; 373 G; 465 T; 0 other;
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                                                                                                  Claim 1; Columns 11-14; 8pp; English.
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Matches 164; Conserv
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AQ051086 nbxb0005a
B1305800 NL_1_M15
BQ908458 T008E03 O
AU094078 AU094078
AU056564 AU056564
B1810180 J001B06 O
                                                                                               March 25, 2003, 19:50:00 ; Search time 2242.74 Seconds (without alignments) 15894.084 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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559.6
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Perfect score:
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	DNA linear GSS 24-MAR-199 y Oryza sativa genomic clone hyta; Embryophyta; Tracheophyta; opsida; Poales; Poaceae; Sequence the Rice Genome ion replaced gi:3325391.	
MENTS	T14 bp  NA sequence.  4501804  diplantae; Streptop Magnoliophyta; Lilli  714) ean, R.A. noting Framework to 98) this sequence vers this sequence vers ity Genomics Instit ity Clemson, SC 29634 88 88 88 93 emson.edu AACAGCTATGACCATG quence start: 31	educe scop:
7 443 20.1 9 429.4 10 418.6 11 416.8 11 416.8 11 416.8 11 416.8 11 416.8 11 416.8 11 416.8 11 416.8 11 41 4 18.8 11 38.9 11 38.9 11 38.4 11 3	N N N N N N N N N N N N N N N N N N N	rrons maru

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NL_1_M15 Drought stress (leaf)
mRNA sequence.
BI305800
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Contact: Reddy AR
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
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                                                                                                                                                                                                                                                                                                                                  genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 KD providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                           /tissue_type="feat"
/lab_host="E. coli DH10B"
/note="Vector: pBeloBAG11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp

Arumuganathan and Barle, 1991). The relatively small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 GCAGAGCATTGTTCTTCTTCTAGCTATTAGTGGTGGGGAATAATGGCTCCCGCCACCA 186
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                                                                                                                                 /clone_lib="CUGI Rice BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 582.6; DB 17;
Pred. No. 7.3e-109;
0; Mismatches 44;
                                      organism-"Oryza sativa"
                                                                             /cultivar="Nipponbare"
                                                                                            /db_xref="taxon:4530"
/clone="nbxb0005E21r"
   location/Qualifiers
                                                         /strain="Japonica'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.5%;
93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 93.0
Matches 654; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                     source
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ORIGIN
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Oryza sativa cDNA clone NL_1_M15 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnollophyta, Lillopsida; Poales; Poaceae, Ehrhartoideae; Oryzeae, Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTs from normalized
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Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,
Ravindrababu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
Stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1413 ACGCCAGCATCGACCTCGTCCTCCATCAAGAGGAAGCTCAGGAAGATCAAGGAGA 1472
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Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-301045
Fax: 0091-40-30104
Fax: 0091-40-30104
Fax: 0091-40-30104
Fax: 0091-40-30104
Fax: 0091-40-30104
Fax: 0091-40-30104
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                                                                                                                                                                                                                                                        599 AATIGGACCCTTATGAAATACCTCTAGAATTCAAATAAACTACATGTCATCTCAATTGCG 658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Plant Sciences, School of Life Sciences University of Hyderabad
                                                                                                                                                                                                                                                                                                                                                                                                                          TATATT-AGTAGTAATTTGCTTCACTAGAATTCTATTTTATAC 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 TATATICAGIGCGAAAICGCIGACIIAGACAICIATICIICIAC 701
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/dev_stage="Mature stage" /note="Vector: pSport2"  BASE COUNT 173 a 194 c 162 g 109 t  ORIGIN  Query Match 24.0%; Score 529; DB 14; Length 638;  Best Local Similarity 89.0%; Pred. No. 6.7e-98;  Matches 615; Conservative 0; Mismatches 0; Indels 76; Gaps 1;	1365   CCAAGCGCACGGCGTACGCGCCGAGGAGGACGCGAGTCCACCTACGCCAGCATCG	Db   64 ACTCGCCTCCATCATCAAGGGAAGCTCAGGAAGATCAAGGAGAGACGAGG 123     QY   1485 TCGCCACCTCAAGGGACCAACCCCCGTCTCCGACTGCCGCCATCATTGCTCGACA 1544	0y         1605         ACGAGGACACGGTGCTCACCAAGGTCTGCAGTCTGATGCATGATGCATATAATCA         1664           bb         244         ACGAGGACACGGTCTCACCA	Db 288 GAGATGCCGCCCTCGGTGGAGGCGATGGACAGCTAGTCAATGTGGACCACAAC 347  Qy 1785 TTCTACGCCTTCAGAGAAGACGGGAGATGAACGCTGTACAAGAGGAAGGA	OY 1905 AACTCTGACCACCACCACCCCTTGCTAGCTCTACACCTCTGCATCACT 1964	OY 2025 TARTCCAAGTGATGAGAGGTCTTTGATT 2055	ACCESSION AU094078 VERSION AU094078 VERSION AU094078 VERSION AU094078 VERSION AU094078 VERSION AU094078 VERSION VERSION VERSION VERSION VERSION VITA VITA VITA VITA VITA VITA VITA VITA
473 TOGGCGCCGAGGACGAGGACACGGTGCTCACCA	DD 429 ACCAAGGIGITCGAGAIGCCGCCGCIGGTGGGGGGGGGGG	Db 309 AAGAGGAAGGAAGGGTTCGGTCTCCTCCTCAAGGGAAGGAA	2013 2013 -129 2073 69 69 2133	Db 9 TGATTTTC 1  RESULT 3  BQ908458 LOCUS BQ908458 638 bp mRNA linear EST 19-AUG-2002  DEFINITION T008503 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone T008503, mRNA sequence.	×	OU A A D O L A A B I A B	Fraz. U086-7-1-180910m.21 Fraz. U086-7-1-180910m.21 Seq primer: M13 forward primer.  Seq primer: M15 forward primer.  Location/Qualifiers  Location/Qualifiers  / GD xref="taxon:4530"  / GD xref="taxon:4530"  / Clone="1008E03"  / Clone="lb="Oryza sativa mature leaf library induced by M.grisea"  / tissue_type="leaf"

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ACCESSION
                                                                                                                                                                                  AUTHORS
                                                                                                                                                                     REFERENCE
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                                                                        VERSION
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                                                                                                                                                                                                                      /clone_lib="Rice panicle at flowering stage"
/dev_stage="flowering stage"
/note="Organ: panicle; Rice cDNA from panicle at flowering
                                                                                                                                                                                                                                                                                                                                                 Η;
                           Contact: Takuji Sasaki
Mational Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Isukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                        1494 TCAAGGGACCAAGCCCCCCTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGACG 1553
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                                                                                                              URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1614 CGGTGCTCACCAAGGTCTGCAGTCTGATGCATGATCAATGCATATAAATCAAATCATTCA 1673
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                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                        1. .597
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76;
                                                                                                                                                                                                                                                                                                                     DB 9; Length 597;
                                                                                                                                                                                                                                                                              4 others
                                                                                                                                                                                                                                                                                                                                                 Indels
Rice cDNA from panicle at flowering stage (2000) Unpublished (2000)
                                                                                                                                                                                                                                                                                                                     Score 491.4; DB 9
Pred. No. 3.3e-90;
                                                                                                                                                                                                                                                                              140 t
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                      305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Emall: tsasakl@abr.affrc.go.jp,
PROJECT ='RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGTGCTCACCA---------
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Location/Qualifiers
                                                                                                                                                                                                                                                                              138 g
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                                                                                                                                                                                                                                                                                                                    22.3%;
87.7%;
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 TITLE
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AUU56564 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica cultivar-group) cDNA clone S20686_2Z, mRNA sequence.
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                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 570)

Yamamoto, K. and Sasaki, T.

Rice cDNA from mature leaf

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa (japonica cultivar-group)"
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/ 153 c 125 g 137 t 7 others
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llarity 98.7%; Pred. No. 1.6e-81;
Conservative 0; Mismatches 6; Indels
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RESULT 6

RESULT 5

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BM420118 522 bp mRNA linear EST 28-JAN-2002 R023H11 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone R023H11, mRNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Buhartoideae; Oryzaee; Oryza.

1 (bases 1 to 52)

Dong, T. T. Li.D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jlang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa"
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                  2037 TGAGAGGTCTTTGATTTTGTCTCCGTGTACATCGATCGACTCTTGACTACTCTG 2096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Raixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Faz: 0086-571-869961525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 20.1%; Score 443; DB 13;
11 Similarity 100.0%; Pred. No. 2.6e-80;
443; Conservative ' 0; Mismatches 0;
                                                                                            2097 ITTAACCAACTGTTTTCGATATATTTATATTAA 2132
                                                                                                                539 TITAACCCACTGTTTTCGATAAAAAAAAAAAA 574
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/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"
a 136 c 122 g 126 t
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Seq primer: M13 forward primer.
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BM420118.1 GI:18386920
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                    EST 02-0CT-2001
                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaeae; Oryzaeae; Oryzaeae; Oryzaeae; Dong, H.T., Lil,D.B., Zhuang, X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jidang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
                                    J001B06 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNa clone J001B06, mRNa sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Oryza sativa"
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                    linear
                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Tel: 0086-571-86892051
Fax: 0086-571-86961525
                  mRNA
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153 c 133 g 133
                    575 bp
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Seq primer: M13 forward primer.
Location/Qualifiers
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                                                                              BI810180
BI810180.1 GI:15857368
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80908495 525 bp mRNA linear EST 19-AUG-2002 1008H05 Oryza sativa mature leaf library induced by M.grisea Oryza
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1 (bases 1 to 525)
Dong-H.T., Lil-D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
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                                                              2002 CTCTAAATATTAC-TAGTATTAATTAATCCAAGTGATGAGAGAGGTCTTTGATTTTGTCT 2060
                                                                                                                                           2061 CCGIGTACAICGAICGATCGACICTIGACIACICIGITITAACCAACIGIITICGAIAIAI 2120
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                                                                                                   378 CICIAAATAITACGIAGIATIAATIAATICCAAGIGAIGAGGGGCTTITGAITTIGICT 437
                                                                                                                                                                Query Match 19.5%; Score 429.4; DB 14; Length 525; Best Local Similarity 99.3%; Pred. No. 1.6e-77; Matches 441; Conservative 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Dong HT
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Bio-rechnology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86891255
Email: htdong@zjuen.zju.edu.cn
Seq primer: M13 forward primer.
                                                                                                                                                                                                                                                                                                                                                                                                     sativa cDNA clone T008H05, mRNA sequence
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/dev_stage="Mature stage"
/note="Vector: pSport2"
134 c 120 g 128
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/db_xref="taxon:4530"
/clone="T008H05"
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Oryza sativa.

Oryza sativa

Dukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Enrartophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryza.

1 (Dasses 1 to 534)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, O.K. and Lou, Y.C.
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                                                                               2062 CGTGTACATCGATCGACTCTTGACTACTCTGTTTAACCAACTGTTTTCGATATATT 2121
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CICIAAAIAIIACIAGIAITAAITAAICCAAGIGAIGAGAGGAGGICITIGAITITGICIC 2061
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Pred. No. 4.7e-78;
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Fax: 0086-571-869961525
Email: htdong@zjuen.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
1. 534
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/tissue_type="leaf"
/dev_stage="Mature stage"
/note="Vector: pSport2"
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/clone="R024B06"
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Best Local Similarity 99.8%;
Matches 443; Conservative
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/clone_lib="Stem library from Oryza sativa (3-5 leaf stage
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Organee; Organee; Organee; Organee;
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
A Gene Expression Screen in Organ sativa
Unpublished (2001)
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GCGAGAGCAGAGCATTGTTCTTCTTCTAGTAGTAGTGGGGGAATAATGGCCTCCCG 190
                                                      CCACCACCACCAGCAATGGCCCTCGCGCCTCCTTCCCATCACCATCACCATCACCATG 240
                                                                                                         191 CCACCACCGCAGCAATGGCCCTCGCGCCCTCCTTCCCATCACCATCACCATG 250
                                                                                                                                                               TCAAGCAGCTGCAGCTCCCTCCGTCTGTCTCCGTCTCCGTGCCCCTCCGGTTCCGGTTTCC 300
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Pred. No. 6e-75;
0; Mismatches 2; Indels 2;
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Fax: 0086-571-86991251
Fax: 0086-571-86901252
Fax: 0086-571-86901252
Fax: 0086-571-8709120
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/dev_stage="3-5 leaf stage"
/note="Vector: pSport2"
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/db_xref="taxon:4530"
/clone="S098C08"
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/clone_lib="gbk279"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
/dev_stage="5 days after pollination"
/dab_bost="E. coll SOLR"
/note="Vector: pBluescript SK(+); Site_l: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5'end with EcoRI and 3' end with Xho I site"
a 161 c 111 g 107 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE230575 460 bp mRNA linear EST 07-JUL-20 99AS79 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa cDNA clone 99AS79, mRNA sequence.
                                                                                                                                                                                                                                                                      2061 CCGIGTACATCGATCGACTCTTGACTACTCTGTTTAACCAACTGTTTTCGATATAT 2120
                                                      CCICTACACCICCIGCAICACCAICCICATIIGCIAATTAITICTAIGCIIGCCAAGAG 2000
                                                                                                                                                             2001 TCTCTAAATATTACTAGTATTAATTAATCCAAGTGATGAGAGAGGGTCTTTGATTTTGTCT 2060
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                                                                               423 CCGTGTACATCGATCGATCGATCTTTGACTCTGTTTAACCAACTGTTTTCGATATAT 482
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1 (bases 1 to 460)
Lee, M.C., Shin, Y.C., Lee, T.H., Jeong, S.H., Kim, J.K., Eun, M.Y.
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Mational Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyungqido, Korea
rel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20.asti.re.kr.
Location/Qualifiers
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Pred. No. 2.6e-75;
0; Mismatches 9
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/cultivar="Milyang23"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                TTATATTATTAATGATTTTTCCAA 2144
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BI811299 516 bp mRNA linear EST 02-0CT-2001 N001C12 Oryza sativa mature leaf library induced by M.grisea Oryza
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1 (bases 1 to 516)
Dong, H.T., Li,D.B., Zhhang, X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,O.K. and Lou,Y.C.
A Gene Expression Screen in Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Oryza sativa mature leaf library induced by M.grisea"
1771 ATGTGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACCGGGGGAGATGAACGTCCTGT 1830
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                                                                                                                                                  1950 CTCCTGCATCACCATCCTCATTTTGCTAATTATTTCTATGCTTGCCCAAGAGTCTCTAAAT 2009
                                                                                                                                                                                                                                                                                                    2010 ATTACTAGTATTAATTAATCCAAGTGATGAGAGGGGTCTTTGATTTTGTCTCCGTGTACA 2069
                                                                                                                                                                                                                                                                                                                                                                           2070 TOGATOGATOGACTCTTGACTACTCTGTTTAACCAACTGTTTTCGATATTTTATTAT 2129
                                                                                                                                                                      241 CTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAGTCTCTAAAT 300
                   1831 ACA-AGAGGAAGGAAGGCTTCGGTCTCATCGTCCCCAAGGGAGACGGTCATCTCCCAC
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Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixunan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
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Pred. No. 1.5e-73;
0; Mismatches 5;
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BI811299
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/dev_stage="Mature stage"
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134 c 114 g 1
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Seq primer: M13 forward primer.
Location/Qualifiers
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/clone="N001C12"
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98,2%;
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Best Local Similarity 98.2°
Matches 436; Conservative
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1 (Dases 1 to 443)

Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jäng, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

M. Gene Expression Screen in Oryza sativa
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               1822 ACGICCIGIACAAGAGGAAGGAAGGCTTCGGTCICAICGICCCAAGGGAGACGGIC 1881
                                                                                       1882 ATCTCCA-CAAGGAGACCATCCCCAACTCTGACCACCACCACCTCCCTTGCTGCTGCTAG 1940
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                                                                                                            535 CCGTGTACATCGATCGACTCTTGACTACTCTGTTTAACC-ACTGTTTTGATATT 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-8699051
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/note="Vector: pSport2"
113 c 93 g 115
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/db_xref="taxon:4530"
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Seg primer: M13 forward primer.
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Matches 426; Conservative
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L010D02 Oryza sativa mature leaf library induced by M.grisea Oryza sativa clone L010D02, mRNA sequence.
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/db_xref="taxon:4530"
/clone="r.010002"
/clone_lib="Oryza sativa mature leaf library induced
                                                       1712 CACCAAGGIGTICGAGAIGCCGCCGCIGICGGIGGAGGAGGCGAIGGAGCAGCIAGIGAA 1771
                                                                                                                                                               1772 TGTGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACGGGGGGGAGATGAACGTCCTGTA 1831
                                                                                                                                                                                                                                                                          1832 CAAGAGGAAGGAAGGAGGCTTCGGTCTCATCGTCCCCAAGGGAGACGGTCATCTCCACAA 1891
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                                                                                       148 IGIGGACCACAACTICTACGCCTTCAGAGACGAGAAGACCGGGGAGATGAACGTCCTGTA, 207
                                                                                                                                                                                                                                                                                                       268 GGAGACCATCCCCAACTCTGACCACCACCACCCCTTGCTGCCTAGCCTCTACACCT 327
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Bio-rechnology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86992051
Fax: 0086-571-86961525
Email: htdong@zjuen.zju.edu.cn
Seq primer: M13 forward primer.
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/note="Vector: pSport2"
140 c 113 g 136
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1 (bases 1 to 539)

Dong, H.T., Li, D.B., Ehuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Ziang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.

A Gene Expression Screen in Oryza sativa
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V006C02 Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNa clone V006C02, mRNa sequence.
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/clone_lib="Oryza sativa mature leaf library induced by
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                                                                                                                                                                                                                                                                                                       1941 CCTCTACACCTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAG 2000
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                                                                                    1761 CAGCTAGTGAATGTGGGACCACAACTTCTACGCCTTCAGAGACGAGAAGACCGGGGAGATG 1820
                                                                                                                    174 AACGTCCTGTACAAGAGGAAGGAAGGCTTCGGTCTCATCGTCCCCAAGGGAGACGGT 233
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  1821 AACGICCIGIACAAGAAGGAAGGAAGGAGGCIICGGICICAICGICCCCAAGGGAGACGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 539;
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Laboratory of Functional Genetics
Blo-technology Institute of Zhejiang University
Raixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Fax: 0086-571-86961525
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Pred. No. 2.9e-71;
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/dev_stage="Mature stage"
/note="Vector: psport2"
144 c 117 g 138
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Seg primer: M13 forward primer.
Location/Qualifiers
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                                                                                       1882 ATCTCCACAAGGAGACCATCCCCAACTCTGACCACCACCACCACCCTTCCCTTGCTGCTGCTAGC 1941
                                                                                                                                                                                                                              1942 CTCTACACCTCCTGCATCACCATCCTCATTTGCTAATTATTTCTATGCTTGCCCAAGAGT 2001
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18.1%; Score 397.4; DB 14; Length 531; 99.5%; Pred. No. 5.6e-71; Live 0; Mismatches 1; Indels 1;
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 Query Match
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March 26, 2003, 04:38:30 ; Search time 54.4409 Seconds (without alignments) 12398.686 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database:
                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 21, Appl Sequence 91, Appl Sequence 538, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 14, Appl Sequence 2, Appli		ngth 1591; ndels 10; Gaps 2; CCAACGTTTGAC 897
28 48 2.2 5970 3 US-09-320-878-21 58 2.2 12730 4 US-09-004-838-91 58 2.2 12730 4 US-09-004-838-91 58 2.2 12730 4 US-09-004-838-91 58 2.2 47.8 2.2 4403765 4 US-09-103-840A-2 58 47.6 2.2 1072 1 US-07-91-096-1 58 47.6 2.2 1072 1 US-07-91-096-1 58 47.4 2.2 2546 1 US-07-951-715A-14 58 47.4 2.2 3546 3 US-08-459-444-14 58 47.4 2.1 3468 1 US-07-951-715A-2 58 47 2.1 3468 2 US-08-459-448A-2 58 47 2.1 3468 2 US-08-459-448A-2 58 47 2.1 3468 2 US-08-459-448A-2 58 47 2.1 3468 3 US-08-459-448A-2 58 47 2.1 3468 3 US-08-459-448A-2 58 47 2.1 3468 3 US-08-459-448A-2 58 48 47 2.1 3468 3 US-08-459-595A-2 58 48 48 47 3 US-08-459-595A-2 58 48 48 48 48 48 48 48 48 48 48 48 48 48	ALIGNMENTS  -3  -3  4pplication US/08728956  5677175  FORMATION: T: Hodges, Thomas K. T: McGee, J. D. INVENTION: Plant Pathogen Induced Proteins F SEQUENCES: SEE: Barnes & Thornburg I 11 S Meridian Indianapolis Indianapolis Indianapolis Indianapolis FREADABLE FORM: TYPE: Barnes & Thornburg  X: USA 46204 disk  READABLE FORM: TYPE: Floppy disk ARADABLE FORM: FREADABLE FORM: TYPE: Floppy disk ARADABLE FORM: FREADABLE FORM: TYPE: PatentIn Release #1.0, Version #1.30  APPLICATION DATA: BREAT INFORMATION: Brear INFORMATION: Brear John P. RATION NUMBER: 3220-26119 UNICATION UNDER: 38,833 NCEATON UNDER: 38,833 NCEATON UNDER: 317,231-7445 NET SEQ ID NO: 3: CHARACTERISTICS: IN FOR SEQ ID NO: 3: CHARACTERISTICS: IN TOTAL: NO SOUNCE: NO SOUNCE:	CRGANISM: Oryza sativa US-08-728-956-3  Query Match Best Local Similarity 66.9%; Pred: No. 8.4e-12; Matches 164; Conservative 0; Mismatches 71; Indels  Qy 841 ATTACTACCTCCATATTTAATGTATGACGCCGTTCACTTTTTGTCCAA

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1009 AAAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAG 1068
                                                                                                                                1069 GGATTATATGGGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTTGGGAGGA 1128
   799 TAAGACAAACGGTCAAACATGTTCTAAAAGTCAAGGGTGTCAAACATTTTGAAACGGAG
                                                                                                                                                                                                                                                                                                              APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANN: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: Foley & Lardner: 1800 Diagonal Road, Suite 500 Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.
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APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463 Patent No. 5670367
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TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                               Patent No. 5670367
GENERAL INFORMATION:
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COUNTRY:
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                                                                                                                                                                                                      1011 AAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTGTCATACATTAAAATACGGAGGG 1070
                                                                                                                                CATCAAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAAA------AAAAA 1010
                                                                                                                                                                                                                            843 IGTTAAATATACTTTCATGTGCACATATAGTTTTACATATTTCACAAATTTTTTGAATA 902
783 CATTITCICITATICAAAAATITAAGIAATITATITATITATITICGIATCATITIGACTCAI 842
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Pred. No. 2.8e-09;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Rice Beta-Glucanase Enzymes TITLE OF INVENTION: and Genes UNGMER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERBNCE/POCKET NUMBER: 2000-0455.30
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/105,390 FILING DATE: Filed herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Filling ton...
CLASSIPICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09105390 Patent No. 6288303
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
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nilarity 64.6%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5: Diskette
IBM Compatible
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ATTORNEY/AGENT INFORMATION:
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CITY: Palo Alto
STATE: CA
COUNTRY: USA
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Best Local Similarity
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US-09-105-390-3
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US-09-105-390-3/c
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Matches 155;
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                   190 CAGCAATGGCCCTCGCCCCCTCCTTCCCATCACCATCACCATCACCATGTCAAGCAGC 249
                                                                                                                                                                   310 CACTGCCTGCTGCTGCCCCACCCACAGCCGCTGCTCGCCGCCGAGGGCCGCCGCGCAGCAGCG 369
                                                                                                                                                                                                                                         370 CCGTGTCCGTGCGGATGTCGTGGGACGGGCCCCTCTCCGCTCCGGCCCTCATTATGCAGG 429
                                                                                            250 TGCAGCTCCCTCCGTCTGTCTCCGTCTCCGTGCCCTCCGCTCCGGTTTCCTTGGCCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                   1424 YYYYYYYYYYYYYGDACCAAATTCTTCTATCTTTAACTACTTGCATAGATAGGTA 1478
                                                                                                                                                                                                                                                                                                                                                                                           Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
WYENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
WYENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1137, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CH 0016/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0V
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 636 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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TELEFAX: 91
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APPLICANT:
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                       1196 GIGGCGGIGCAGCIGAAIGAGAAGGIGAAGGAGCACAICGAGGAGAAAGGCGGGGAGAGCA 1255
                                                                                                                                                                         130 GAGCATIGITCITCITCITCIAGCIATTAGIGGTGGGGGAATAAIGGCICCCGCCACCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                          Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F. APPLICANT: SCHEIFLINGER, F. APPLICANT: STAKNER, F. G.
TITLE OF INVERTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                 1183 RRREARRERERERERERERERERER 1149
                                                                                                                                                                                                                        1256 GIGGCGAAGCACAGCCITGTGAAGGAGGTGGA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE, DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICATION NUMBER: EP 91 114 300.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
XIP: 22313-0299
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                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-232-463-14
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REGISTRATION NUMBER:
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STREET: Two Pri
CITY: Chicago
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                                                                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     860 AATGTATGACGCCGTTCACTTTTGTCCAACGTTTGACCATTCGTCTTATTAAAAAAA 919
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                                                                                                                                                                                                                                                              560 GATTCATTATCATATATATGATTATAGGTAATGCTAGAAAATCTTATAACCTGAAACAGA 619
                                                                                                                                                                                                                                                                                                     198 --TTAATATGAATACTATTTAGTCTATGTTCAAATTTTAAATTTAGTTATTAAAATATTAT 255
                                                                                                                                                                                                                                                                                                                                            620 GGGAGTATATATATATTCGGTAATGGAACTAGAGTATTTGTTTTATTAATTGGACCTTTAT 679
                                                                                                                                                                                                                                                                                                                                                                                                                         680 GAAATACTAGTAGAATTCAACGAAACTACATTCTTCTTTATTGGTTATATTAGTAAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 IIGCIICACIAGAAITCIAITTTAIACTAGAGAGAITAAAAATTAITACAAAACIAACIG 799
                                                                                                                                                                                 Gaps
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                                                                                                                                            3;
                                                                                                       Length 636;
                                                                                                   Score 62.2; DB 4; Length 63
Pred. No. 3.1e-05;
0; Mismatches 258; Indels
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Patent No. 5677175
GENERAL INFORMATION:
APPLICANT: Hodges, Thomas K.
APPLICANT: McGee, J. D.
TITLE OF INFORTION: Plant Pathogen Induced Proteins
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/728,956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
      DNA (genomic)
                                                                                                     Query Match 2.8%;
Best Local Similarity 46.8%;
Matches 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
                                       PAG1692RP
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MOLECULE TYPE: DI
ORIGINAL SOURCE:
ORGANISM: PAG1(
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ZIP: 46204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                              US-08-998-416-1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-728-956-3/c
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996 ATTTGCAAAAAAAAAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACA 1055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1591;
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APPLICANT: Xia, Yiji
TITLE DE INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61.8; DB 1;
Pred. No. 5.9e-05;
0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Leydig, Voit & Mayer, Ltd.
Two Prudential Plaza, Suite 4900
                    3220-26119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1056 TTAAAATACGGAGGGATTATATG 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                743 TTTTGAAACGGAGGGAGTATTTG 721
38,833
               REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)231-7745
TELEFAX: (317)231-7433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nikolau, Basil J.
                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.8%;
                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
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                                                                                                                                                                      LENGTH: 1591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Oryza sativa
US-08-728-956-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 55.5
Matches 146; Conservative
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COUNTRY: US
ZIP: 60601-6780
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
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FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
XY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
FELECOMMUNICATION INFORMATION:
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Pohlmann, Rainer
Steiner, Sabine
                                                                                                                                                                                                                                                             2.7%;
                                                                                  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 57.7
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                           TELEFAX: 650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-105-390-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                         TELEPHONE:
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AA 897
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APPLICANT:
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STATE:
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                                                                                                                                                                                                                                                                                                                                             2.7%; Score 59.6; DB 3; Length 1138; 51.9%; Pred. No. 0.00016; tive 0; Mismatches 124; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
FAPLICANT: ROCATIONEZ, RAYMONG
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
TITLE OF SEQUENCES: 66
CORRESSED Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTERS. 2007.

COPERATING SISTEM: DOS
SOFTWARE: FRASERY for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NOBABR: 60/050,675
FILING DATE: 25-UDN-97
ATTORNEY/AGENT INFORMATION:
                                                         REFERENCE/DOCKET NÜMBER: 7138
TELEPROMUNICATION INFORMATION:
TELEPROME: (312) 616-5600
TELEPROME: (312) 616-5700
INFORMATION FOR ENQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
ELENGTH: 1138 base pairs
                    NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
                                                                                                                                                                                                                                                    TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1615 GGTGCTCACCAAGGTCTG 1632
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 51.9
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                                    LENGTH: 1138 base pai
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 350 Cam!
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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945 TGACTTGATTCGTCATCAAATATTTTTTAAGCATGACATAAACATTTTCATATTTGCAAA 1004
                                                                                                                                          885 ICCAACGITIGACCATICGICITAIDAAAAAAATIAIGIAICIATIATTATTATTA 944
                                                                                                                                                                                                                                                                       776 GAACAIGITIGACCGITIGICITATICAAAAAAAAATIGIGAAAIAIGITAAAITATAIGI 835
                                                                                                                                                                                                                                                                                                                                                                             825 TAIGGACCIATTACTATTACTACCTCCATATTTAATGIATGACGCCGTTCACTTTTTG 884
                                                           Gaps
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     Length 2317;
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                                                        Indels
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Score 58.8; DB 4;
Pred. No. 0.00035;
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ORGANISM: Artificial Sequence
                                   OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-998-416-288
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                                                                        ) OTHER INFOR
US-09-197-649-7
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APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
ERALIER RELING DATE: 1998-10-31
ERRLIER APPLICATION NUMBER: 07/829,461
ERRLIER APPLICATION NUMBER: 07/739,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 GAAATACTAGTAGAATICAACGAAACTACATTCTICTTTATIGGTTATATTAGTAGTAAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           860 AAIGIAIGACGCCGIICACITITIGICCAACGITIGACCAITCGICITAITAAAAAAA 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        920 TAIGTATCTATTATTTATTATATGACTTGATTCGTCATCAATATTTTTAAGCATG 979
                                                                                                                                                                                                                                                                                                560 GATICATTAICATATATATGATTATAGGTAATGCTAGAAAATCTTATAACCTGAAACAGA 619
                                                                                                                                                                                                                                                                                                                                                                                                           620 GGGAGTATATAATTCGGTAATGGAACTAGAGTATTTGTTTTATTAATTGGACCTTTAT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 ATTGTAAATTATTATT-TTTATTAATATCTATTTTTATAATATTATGTTGATTATA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 ITAITTAACTITITATAAGAAITAITAATAAAAITTAAATITTAACTITAAITITCITAITAI 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      800 TATACCCGTTGCAACGGAATAGTAATATGGACCTATTACTTATTACTACCTCCATATTTT
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                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                            Length 615;
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                                                                                                                                                                                                                        Score 58.4; DB 4; Pred. No. 0.00023; 0; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09197649
Patent No. 6194550
RENERAL INFORMATION
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
                     186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1991-08-01
                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                          Query Match 2.7%;
Best Local Similarity 47.9%;
Matches 230; Conservative
               INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Ver. 2.0
 919-541-8689
                                                                                                                                                               ; ORGANISM: PAG1074RP
US-08-998-416-186
TELEFAX:
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US-09-197-649-7
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LENGTH: 39
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CTCCTCCATCATCAAGAGGAAGCTCAGGAAGATCAAGGAGAAGAAGGAGACCGACGTCCGCCA 1491
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                                                                                                                                                                                                                                                  1372 CCACGGCGTCATCCGCGCGCGGAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCAAGGGGACCAAGCCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGA 1551
                                                                                                                                                                                                                                                                                 Gaps
Description of Artificial Sequence: Sequence having a 120 repeat of ACG flanked by fixed fragments having Nool restriction sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Schiner, Sabine
APPLICANT: Moriems, Sabine
APPLICANT: Moriems, Christine
APPLICANT: Mechtle,
APPLICANT: Mechtle, Philipp
APPLICANT: Rechtle, Philipp
APPLICANT: Relschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCES: 1152
                                                                                                                                    2.6%; Score 56.6; DB 4; Length 390; 51.0%; Pred. No. 0.00048; tive 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
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ATTORNEY/AGENT INFORMATION:
NAME: Me1gs, J. TIMOCHATION:
RESISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: FF/5-30306/A/CGC1976
TELEPHONE: 919-541-8689
TELEFAR: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 288, Application US/08998416 Patent No. 6239264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 134; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                       Query Match
Best Local Similarity
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Sequence 3, Application US/08213419B Patent No. 6333406
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ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.4%;
Best Local Similarity 47.1%;
Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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US-08-781-891-209
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LENGIH: 6124
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                                                                                                                                                                                                                                                                                                                                                                                                                                        198 --TTAATATGAATACTATTTAGTCTATGTTCAAATTTTAAATTAGTTATTAAATTATTAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 GGGAGTATATATAATTCGGTAATGGAACTAGAGTATTTGTTTATTAATTGGACCTTTAT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         680 GAAATACTAGTAGAATTCAACGAAACTACATTCTTCTTATTGGTTATTAGTAGTAAT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 TTATTAATTGTTTAAAAAAAAATAATTTTTTAATAAAAGATTTAATTTAATT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  800 TATACCCGTTGCAACGGAATAGTAATATGGACCTATTACTTATTACTACCTCCATATT-T 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         859 TAATGTATGACGCCGTTCACTTTTGTCCAACGTTTGACCATTCGTCTTATAAAAAA 918
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                                                                                                                                                                                                                                                                                                             740 TIGCTICACIAGAATICIATITIATACIAGAGATITAAAAATTATTACAAAACIAACIG 799
                                                                                                                                                                                                                            2.5%; Score 56; DB 4; Length 837; ilarity 47.4%; Pred. No. 0.00095; Conservative 0; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 209, Application US/08781891

Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Chang-En
APPLICANT: W, Chang-En
APPLICANT: Willigan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
288:
                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                  LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
; INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                               ORGANISM: PAG1241RP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 GIAGITAAAAT 627
                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 233; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washington
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US-08-781-891-209/c
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL GENERAL GENER ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION:
GENERAL JUI-0020NCP
CURRENT EPPLICATION UNMERR: US/08/213,419B
CURRENT PAPLICATION UNMERR: US 07/870,506
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR APPLICATION NUMBER: 20
SPIOR FILING DATE: 1992-04-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VOIL 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1067 AGGGATTATATGGGATAGCTACAGTAGCAGAGTCATGATAAAGTAGTAATGTGTTGGGAG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1007 AAAAAAACGAAIGGICAAAIGIITAGICGAAAAGICAAIGGIGICAIACAIIAAAAIIACGG 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1127 GAGCGGTAGAGCGTTGTGTGGAAAATAAAGATGGGAATGGAATGGAATGAAAAGCGTAC 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1187 GTGCGTGGCGTGGCGGTGCAGCTGAATGAGAAGGTGAAGGAGCACATCGAGGAGAAGGCG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 AAACACACAATAAGAAAATCCAGACCCTGTAAATGATTGAATGAGTAAAACACAGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52.8; DB 3; Length 51259;
Pred. No. 0.037;
0; Mismatches 182; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1247 GGGAGAGCAGTGGCGAAGCACAGCCTTGTGAAGGAGGTGGA 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 GGCCAGGAGGAGGAGGAGGAGGAGGAGCAGCAGGAGCAGGA 63
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFRANE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NORBER: US/08/781,891
FLING DATE: 27-DDC-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                        REFERENCE TO INFORMATION:
TELECHONIN (CATLON INFORMATION:
TELEPRAN: (206) 622-490
TELEFRAN: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
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TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERTTHROCITE BINDING PROTEINS NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1353 TCACTCTCTTCACCAAGGGCCACGGGGTCATCCGCGCGAGGAGGACGCCGAGTCCACCT 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1413 ACGCCAGCATCGACCTCGCCTCCTCATCAAGAGGAAGCTCAGGAAGATCAAGGAGA 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1473 AGGAGACCGACGTCCGCCACCTCAAGGGGACCAAGCCCCCCGTCTCCGACTGGCCGCCAT 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1533 CATTGCTCGACAACAACGACGACGACGCCCAGGCCCAGCTCAAGGATCTGGAGGAGGCCG 1592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.3%; Score 50.8; DB 3; Length 1 Best Local Similarity 52.3%; Pred. No. 0.018; Matches 137; Conservative 0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                   0665-0007.30
MBER: US/09/023,173
13-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/038,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1593 TCGGCGCCGAGGACGACAC 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 CCCCCCCCCCAACGAGGCCAC 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-Zhaun
APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                          FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42995
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                         LENGTH: 1140 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                             TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       California
                                                                                                                                                                                                                                                                                                                                                                                         linear
                          FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-023-173-4
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1227 GGTATACTTCATATAAATCATATTAAGGATAAATGTATTTTAATAAAATATTACATGAAC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1287 ATAAAATTAGTAAGACTTTATGATGGAAAAGCAATATTAATTCATGAGCCTTAATATT 1346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 AUTHAUTUTATIAGACUTGAUTICGICATCAAATAITUTTTAAGCAIGACAIAAACATT 991
                                                                                                                                                                                                                                                                                 929 ATATATATATTTTTAAATATTTTAAAAGAGAAAAGAATGAAAAATGTACATATATGTA 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        753 AITCTATITTATACTAGAGAGTTAAAAATTATTACAAAACTAACTGTATACCGTTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 ACGGAATAGTAATATGGACCTATTACTTATTACTACCTCCATATTTTAATG-TATGACGC
                                                                                                                                                                                                   Length 6124;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09023173
Patent No. 6066781
GENERAL INFORMATION:
APPLICANT: Sutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of Mature Proteins
TITLE OF INVENTION: in Plants
                                                                                                                                                                                               Score 51.2; DB 4; Pred. No. 0.031; 0; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CIPY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 992 TCATATTTGCAAAAAAAAAAAGGAA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1347 TTGTTAATATAAGAATAAATAAAAA 1372
                                                                                                                                                                                               2.3%;
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
  (2407)..(2439)
                                            (2598)..(3404)
                                                                                      (3580)..(3720)
                                                                                                          CDS
(3850)..(5835)
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235; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                  CDS
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                                                                                                                                ; LOCATION: (3
US-08-213-419B-3
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US-09-023-173-4
      LOCATION:
                                                                                                                                                                                                 Query Match
Best Local
                          NAME/KEY:
                                                                  NAME/KEY:
                                                                                      LOCATION:
                                                                                                            NAME/KEY
                                                                                                                                                                                                                                         Matches
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16111 TATATATATATATATATATATATATATGTATGTGTAAATGTGTATGTAGTTATGGGTAT 16052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        596 GAAAATCTTATAACCTGAAACAGGGGGGGTATATAATTCGGTAATGGAACTAGAGTAT 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  656 ITGITITATTAATTGGACCITTATGAAATACTAGTAGAATTCAACGAAACTACATTCTTC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 716 TITATIGGITATATTAGTAGTAATTIGCTICACTAGAATTCTATTITATACT - AGAGAG 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 774 ATTABABATTATTACAAAACTAACTGTATACCCGTTGCAACGGAATAGTAATATGGACCT 833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 TICCCIGGAATITICCTICGITICATATIATAAGGITITICTAGCATTACTCATATICACAT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834 ATTACTTATTACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTGTCCAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match. 2.3%; Score 50.6; DB 2; Length 19124; Best Local Similarity 44.8%; Pred. No. 0.074; Matches 236; Conservative 0; Mismatches 289; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    954 TCGTCATCAAATATTTTTAAGCATGACATAAACATTTTCATATTTG 1000
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
GLASSIPTOTATION: 435
ACTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE:
US-08-487-826B-13
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Search completed: March 26, 2003, 13:11:56 Job time : 246.441 secs

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GenCore version 5.1.4_p5_4578

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 05:23:30 ; Search time 121.358 Seconds

(without alignments)

15433.627 Million cell updates/sec

ritle: US-09-702-134-7212_COPY_10200_12400

Perfect score: 2201

Sequence: 1 cgtcgttcgttttggcatc......tagcttggcttttgctgta 2201

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0

Maximum Match 0%

Post-processing: Minimum Match 10%

Listing first 415 summaries
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Database: published Applications\_NA:\*

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
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14: /cgn2\_6/ptodata/1/pubpna/US0\_PUBCOMB.seq:\*
14: /cgn2\_6/ptodata/1/pubpna/US0\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 859, App	Sequence 606, App	Sequence 308, App			Sequence 859, App	Sequence 862, App	Sequence 2, Appli	Sequence 832, App	Sequence 53, Appl	Sequence 7, Appli	Sequence 4849, Ap	Sequence 9, Appli	Sequence 1, Appli	ience 35, Appl	Sequence 3436, Ap	Sequence 5785, Ap	Sequence 3, Appli	
	Desci	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sedi	Sedi	Sec	Sedi	Sedi	Sec	Sec	-
	ΠD	US-09-887-576-859	US-09-770-791-606	US-09-770-149-308	US-09-921-992-2	US-09-887-576-832	US-09-887-576-859	US-09-887-576-862	US-09-921-992-2	US-09-887-576-832	US-09-791-171-63	US-09-790-399-7	US-09-938-842A-4849	US-09-858-525A-9	US-09-790-988-1	US-09-927-827-35	US-09-938-842A-3436	US-09-960-352-5785	US-09-927-112-3	
	DB	10	10	10	10	10	10	10	10	10	10	10	Q	Q	10	6	6	10	10	
	Query Match Length DB	2000	356	689	33675	2000	2000	2000	33675	2000	550	390	2000	2520	640681	4880	2000	516	3624	
dР	Query Match	6.5	5.7	5.0	4.	4.4	4.4	4.2	3.3	3.3	2.7	2.6	2.4	2.3	2.3	2.2	2.3	2.2	2.2	
	Score	143.6	124.4	110.2	100	97.4	96.6	92.8	72.6	72.4	59.6	56.6	53.4	51.6	51.4	49.2	49	48.8	48.8	
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	Result No.	υ	O		O	O							O			,				

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Gaps

Score 143.6; DB 10; Length 2000; Pred. No. 5e-24; 0; Mismatches 44; Indels 10;

Query Match 6.5%; Best Local Similarity 79.5%; Matches 210; Conservative ( 822 TAATAIGGACCIAITACTIATTACTACCICCAPATITTAAIGIAIGACGCCGITCACTIT 881

20 AG AG

Sequence 4225, Ap Sequence 4225, Ap Sequence 41100, Ap Sequence 40, Appl Sequence 40, Appl Sequence 2017, Ap Sequence 2717, Ap Sequence 114, Appl Sequence 154, Appl Sequence 2, Appl Sequence 33, Appl Sequence 33, Appl Sequence 34, Appl Sequence 34, Appl Sequence 34, Appl Sequence 37, Appl Sequence 68, Appl Sequence 714, Appl	expression
US-09-960-352-5558 US-09-938-842A-4225 US-09-969-373-1100 US-09-968-373-1100 US-09-861-289-40 US-09-861-289-40 US-09-864-76-6203 US-09-864-76-6203 US-09-864-76-6203 US-09-98-462-14 US-09-98-462-14 US-09-98-462-4 US-09-98-462-4 US-09-98-462-4 US-09-98-462-4 US-09-98-462-4 US-09-98-462-4 US-09-98-462-2 US-09-98-462-4 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-462-2 US-09-98-3 US-09-98-3 US-09-98-3 US-09-98-3 US-09-98-3 US-09-771-208-20 US-09-452-239-37 US-09-452-239-37 US-09-452-239-37 US-09-452-239-37 US-09-452-239-37	ALIGNMENTS 09887576 s for regulation of plant US/09/887,576 6-25 60/213,848 60/213,848 3 60/214,087 3 80/258,692 9 5 Version 4.0
431 10 2.2 1729 9 2.2 2083 10 2.2 2087 9 2.2 2087 9 2.2 2787 10 2.2 2787 10 2.2 3787 10 2.2 3787 9 2.2 3786 9 2.3 3756 9 2.1 3468 9 2.1 474 10 2.1 56158 9 2.1 56158 9 2.1 65168 9 2.1 6	lication US/ 0144047A1 0N: Trth, P. n, D. 9, H. T. B. A. S. N Eret ON: Promoter 1360.0013G1 1360.0013G1 1360.0013G1 1360.0013G1 ATE: 2001-06-2 E: 2000-06-2 N NUMBER: US E: 2000-12-2 N NUMBER: US E: 2000-13-2 N NUMBER: US E: 2000-13-2 NUMBER: US E: 2000-13-2 NUMBER: US E: 2000-13-2 NUMBER: US E: 2000-13-
20 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1  US-09-887-576-859/c  Sequence 859, Applicatio, Sequence 850, Applicatio, GENERAL INFORMATION: APPLICANT: Bundworth, P. APPLICANT: Chang, H. APPLICANT: Chang, H. APPLICANT: Chang, H. APPLICANT: Chang, H. APPLICANT: Cooper, Bre APPLICANT: Cooper, Bre APPLICANT: Han, B. APPLICANT: Han, B. APPLICANT: Cooper, Bre TITLE OF INVENTION: Pro CURRENT PLING DATE: 2000 CURRENT APPLICATION NUMBE PRIOR FILING DATE: 2000 PRIOR APPLICATION NUMBE PRIOR FILING DATE: 2000 PRIOR FILING DATE:
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SEQ ID NO 308
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                  1472 TTATTGTGACTTGATTTATCATCAAATGTTCTTTAAGCATGATATAAGTATTTTTGTATT 1413
                                                                        999 IGCAAAAAAAA-----AAAACGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCA 1051
                                                                                             1214 GAGAAGGTGAAGGAGCACATCGAGGAGAAGGCGGGGAGAGCCAGTGGCGAAGCACACCAG 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGACGCCGAGTCCACCTACGCCAGCATCGACCTCGCCTCCTCCATCATCAAGAGGAAG 1453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hoffman, Neil
APPLICANT: Hoffman, Neil
APPLICANT: Horban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT APPLICATION NUMBER: US/09/770,791
PRIOR APPLICATION NUMBER: 60/118,480
PRIOR FILING DATE: 2000-01-07-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAGGAAGATCAAGGAGAAGGAGACCGAC 1483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                     1352 TACATTAAATATGGAGGAGTAT 1329
                                                                                                                                            1052 TACATTAAAATACGGAGGGATTAT 1075
                                                                                                                                                                                                                                                                       Sequence 606, Application US/09770791
Patent No. US20020062014A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jorn
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Raas, William David
Garcia, Carlos A.
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                                                                                                                                                                                                                                                                                                                                              An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
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Rameaka, Joshua G.
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Slader, Ted
Davis, Keith R.
Allen, Keith
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APPLICANT:
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APPLICANT:
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APPLICANT:
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1274 CTTGTGAAGGAGGTGGACGTGCGCCTCTCCGCCCGCGGTGGCGAGGTCAGCCGAGGTCCC 1333
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APPLICANT: Ricker, Maja
APPLICANT: Slader, Ted
APPLICANT: Slader, Ted
APPLICANT: Slader, Ted
APPLICANT: Allen, Keith R.
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Labliana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,506
PRIOR APPLICATION NUMBER: 60/178,506
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.0%; Score 110.2; DB 10;
Best Local Similarity 62.2%; Pred. No. 2.2e-16;
Matches 163; Conservative 0; Mismatches 99;
US/09770149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)...(689)
; OTHER INFORMATION: n - A,T,C or G
US-09-770-149-308
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Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
Davis, Keith R.
                                                            Gorlach, Jorn
An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                       Yu, Yang
Rameaka, Joshua G.
  Sequence 308, Application
Patent No. US20020059663A1
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LOCATION: (1)...(689)
                                            GENERAL INFORMATION:
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RESULT 4

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REFERENCE: 1360.001US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1016 AATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATACGGAGGGATTAT 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       843 TACTACCTCCATATTTTAATGTATGACGCCGTTCACTTTTTGTCCAACGTTTGACCATTC 902
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LOCATION: (6224)...(7019), (7163)...(7269), (7344)...(7444), (7525)...(7634)
LOCATION: (7694)...(7813), (7923)...(8153)...(8253)...(8159), (8155)...(8159)
LOCATION: (9012)...(9071), (9163)...(9225), (9328)...(9472), (9589)...(9730)
LOCATION: (9931)...(10028), (10134)...(10292), (10694)...(10798),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963 AATATTTTTAAGCAIGACATAAACATTTTCATATTTGCAAAAA------AAAAAAACG
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Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
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                                                                                                                                                                                                                                    APPLICANT: Venkatramesh, Mylavazapu
TITLE OF INVENTION: Methyl-D-Erythritol Phosphate Pathway (
FILE REPERENCE: 16516.10/735-21(51897)US
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR PELING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION; (1.33675)
; OTHER INFORMATION: unsure at all n locations
US-09-921-992-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                            Campos, Narciso;
Rodriguez-Concepcion, Manuel;
Rohmer, Michel;
                                                                                                                                                                             Seeman, Myriam;
Valentin, Henry E.;
Venkatesh, Tyamagondlu V.;
                   Sequence 2, Application US/09921992
Patent No. US20020069426A1
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                                                            GENERAL INFORMATION:
APPLICANT: Boronat, Albert,
APPLICANT: Campos, Narciso
APPLICANT: Rodriguez-Conce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 67.6
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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US-09-887-576-832/c
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1662 TICIATCATITGATICATTATTAAATATATTITTCCGTATATATATATATGTTTTCATATITC 1603
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APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Wand, X.
APPLICANT: Cooper, Bret
APPLICANT: Cooper, Bret
CURRENT - REFERENCE: 1360.001019
FILE REFERENCE: 1360.001019
CURRENT - REPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastERD for Windows Version 4.0
: LENGHH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  940 TATTATGACTTGATTCGTCATCAATATTTTTAAGCATGACATAAACATTTTCATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 4.4%; Score 97.4; DB 10; Best Local Similarity 63.1%; Pred. No. 5.4e-13; Matches 185; Conservative 0; Mismatches 101;
CURRENT APPLICATION NUMBER: 08/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 859, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Oryza sativa
US-09-887-576-832
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4.4%; Score 96.6; DB 10; Length 2000;

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| 1327 AT 1328
                          1076 AT
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                                                                                                                                                                              1381 IGACCATICGICITALICAAAITITITAIGCAAATACAAAAATACITAIAIACATGCITAA 1440
                                                                                                                                                                                                                                            1004 AAAAAAAAAAGGAATGGTCAAATGTTAGTCGAAAAGTCAATGGTGTCATACATTAAAATA 1063
                                                                                                                                                                                                                                                                                                                         1501 TITAATAAAAGGAAAGGTCAAACGTITATTAAAAAGTCAACTGCGTTATACATTAAAAATA 1560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1147 CGTCTTATTCTAAAATTTAAGTAATTATTAATTCTTTTCCTATCATTGATTCATCGTT 1206
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                                                                                                                                        894 TGACCATTCGICTTATTAAAAAATTATGTAICT-----ATTATTTATTATTATGAC 948
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Ban, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE APPLICANT: Cooper, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2%; Score 92.8; DB 10; Length 2000; 67.4%; Pred. No. 6.8e-12; ive 0; Mismatches 72; Indels 7;
                        Indels
    8.4e-13;
ches 74;
    Pred. No. 8.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FESSLSEQ for Windows Version 4.0
SEQ ID NO 862
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 201-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 862, Application US/09887576 Patent No. US20020144047Al
67.1%;
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Best Local Similarity 67.4
Matches 163; Conservative
                    171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Oryza sativa
US-09-887-576-862
    Similarity
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    Best Local
Matches 17
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16640 ATCITATTCAAAAATTITTGTGAAATATATAAAACTATATGTATACATAAAGTATATT 16699
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(7644)..(7813),(7923)..(8153),(8253)..(8369),(8515)..(8589),
(9012)..(9071),(9163)..(9225),(9328)..(9472),(9589)..(9730),
(9951)..(10038).(10134)..(10293),(10684)..(10798),
                                                                                                                                                                       APPLICANT: Rodriguez-Concepcion, Manuel;
APPLICANT: Rohmer, Michel;
APPLICANT: Rohmer, Michel;
APPLICANT: Seeman, Myriam;
APPLICANT: Valentin, Henry E.;
APPLICANT: Venkatesh, Tyamagondlu V.;
APPLICANT: Venkatramesh, Mylavarapu
TILLE OF INVENTION: Methyl D-Errythritol Phosphate Pathway Genes
FILE REFERENCE: 16516.107/35-21(51897)US
CURRENT APPLICATION NUMBER: US/09/921,992
CURRENT FILING DATE: 2001-08-06
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; Score 72.6; DB 10; Length 33675; Similarity 59.2%; Pred. No. 3.3e-06; Conservative 0; Mismatches 94; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IOCATION: (1..33675)
; OTHER INFORMATION: unsure at all n locations
US-09-921-992-2
                                                                                                                                                     Campos, Narciso;
Rodriguez-Concepcion, Manuel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 832, Application US/05887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
    APPLICANT: Budworth, P.
US-09-921-992-2
; Sequence 2, Application US/09921992
; Patent No. US20020069426A1
                                                                                                                      APPLICANT: Boronat, Albert;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Oryza sativa
                                                                                           GENERAL INFORMATION
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LOCATION: (9012).
LOCATION: (9951).
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Matches 145;
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US-09-790-399-7
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APPLICANT: RASMISSEN, Peter Birk
APPLICANT: RASMISSEN, Peter Birk
APPLICANT: RELDINGH, Karin
APPLICANT: FICANO, Walter
TITLE OF INVENTION: DERIVED FRAGMENTS AND POLYPEPTIDE FRAGMENTS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
CURRENT APPLICATION NUMBER: US/09/791,171
CURRENT PILING DATE: 2001-02-20
                                                                                                  APPLICANT: COOPET, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE REPERBERBE. 1360.00103.
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
SOFUMBER OF SEQ ID NOS: 875
SOFTWARE FASTER FASTER FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.3%; Score 72.4; DB 10; Length 2000; Best Local Similarity 58.3%; Pred. No. 5.1e-07; Matches 148; Conservative 0; Mismatches 101; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/050,739
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 0376/97
PRIOR FILING DATE: 1997-04-02
PRIOR RELING DATE: 1997-11-10
PRIOR PLING DATE: 1997-11-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/09791171 Patent No. US20020094336A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ANDERSEN, Peter APPLICANT: NIELSEN, Rikke
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Brown, D.
Chang, H.
                                       Zhu, T.
Han, B.
Wang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 832
                                                                                        APPLICANT:
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APPLICANT:
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| FALCHIA NO. SZOVZZUZBUJBUJALI
| STRERAL INDORMATION:
| APPLICANT: Gold, Larry
| APPLICANT: Tuerk, Carig
| APPLICANT: Tuerk, Carig
| APPLICANT: Pribnow, David
| APPLICANT: Pribnow, David
| APPLICANT: Pribnow, David
| TILE OF INTENTION: Systematic Polypeptide Evolution by Reverse Translation
| TILE OF INTENTION: Systematic Polypeptide Evolution by Reverse Translation
| TILE OF INTENTION NUMBER: US/09/790, 399
| CURRENT FILING DATE: 2001-02-22
| PRIOR APPLICATION NUMBER: 09/19/649
| PRIOR PLING DATE: 1992-01-31
| PRIOR PLING DATE: 1992-01-31
| PRIOR PLING DATE: 1991-08-01
| PRIOR PLING DATE: 1991-08-01
| PRIOR PLING DATE: 1990-08-02
| NUMBER OF SEQ ID NOS: 26
| SOFTWARE: Patentin Ver: 2.0
| SEQ ID NO S.
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                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 59.6; DB 10; Length 550; 50.3%; Pred. No. 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                490 GTAGCTCTGCCCAGCGTGTTCTTTTGCGTCTGCTCGGCCCGTAGCGAACA 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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51.0%; Pred. No. 0.00096;
tive 0; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 144;
                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium tuberculosis
PRIOR FILING DATE: 1997-04-18
PRIOR APPLICATION NUMBER: 60/070,488
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 173
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09790399 Patent No. US20020038000A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 51.0 Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.3 Matches 145; Conservative
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1326 GAGGTCCCAAGATTTGCAGGTGCGAGATCACTCTTCACCAAGCGCCACGGCGTCATCC 1385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 AGTOCTCCGCCACTGGTGACTTCACCTTCAAGCTGTCCGACGACGAGAACGCCATCATCG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 AGGCCAGCTGCTGCAGATCAAGATCCAGTCCGACGCCGTGCACATCGACA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 ACAAGATCTTCAAGAGCTGAAGCTGTTCAAGATCGACTCCCAGAACCACTCCCAGCAGG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 ACACCCTCGTGGACCAGAAGCACCAGAGTACCACTCCATCCGCTGGATCGGCCTGATCC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     457 TGCAGCAGGACGAGCTGAGGAACCCAGAGTTCAACAAGAAGGAGACCCAGGTGTTCCTGA 516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: modified DNA encoding ISPlA protein
                                                                                                                                                                                                                               Sequence 9, Application US/09858525A; Sequence 9, Application US/09858525A; Squence 9, Application No. US20020199215A1
GENERAL INFORMATION:
APPLICANT: ARNAUT, Greta
APPLICANT: VAN RIE, Jercen
APPLICANT: DAMME, Nicole
TITLE OF INVENTION: No. US20020199215A1e1 Toxins
FILE REFERENCE: 011565-077
CURRENT FILING DATE: 2001-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/573,872
PRIOR FILING DATE: 2000-05-18
NUMBER. OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
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                                                                                                                              1569 AATTTAATACGATTTAAATAA 1549
                                                                               ACATITICATATITICCAAAAA 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (3)..(2510)
US-09-858-525A-9
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US-09-858-525A-9
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US-09-790-988-1
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GENERAL INCOMPATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joef

APPLICANT: Kreps, Joef

APPLICANT: And Mang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILLE REFERENCE: SCRIP1300-2

CURRENT APPLICATION NUMBER: US 60/227, 866

PRIOR APPLICATION NUMBER: US 60/264, 647

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-06

PRIOR FILING DATE: 2001-06-22

NUMBER OF SOO ID NOS: 5379
                                                                                                      1552 CGACGACGCCCAGGCCCAGCTCAAGGATCTGGAGGAGGCCGTCGGCGCCGAGGACGAGGA 1611
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                                                                                                                                                                                                   1492 CCTCAAGGGGACCAAGCCCCCCGTCTCCGACTGGCCGCCATCATTGCTCGACAACAACGA 1551
     1372 CCACGGCGTCATCCGCGCGGAGGACGACGCCGAGTCCACCTACGCCAGCATCGACCTCGC 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         686 CTAGTAGAATTCAACGAAACTACATTCTTCTTTATTGGTTATTAGTAGTAATTTGCTT 745
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                                    626 AFATATAATTCGGTAATGGAACTAGAGTATTTGTTTTTTTAATTGGACCTTTATGAAATA 685
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Pred. No. 0.018;
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                                                                                                                                                                                                                                                                                                                                                                                                 1612 CACGGTGCTCACCAAGGTCTGCA 1634
                                                                                                                                                                                                                                                                                                                                                                                                                              368 CGCCATGGTTGCGATGGTCAGGA 390
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Best Local Similarity.
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US-09-938-842A-4849/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D 353539 ATABITITITATITATITAGAATTAACATTAAGTATTGAATACATTITGATATTT 353598
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                                                                                                                                                                                                                                                                                                                                                 Length 640681;
                                APPLICANT: HATTORI, MASHIRA
APPLICANT: SAKAKI, YOSHITUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT PELLOR APPLICATION NUMBER: 108/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                             Score 51.4; DB 10;
Pred. No. 3.1;
0; Mismatches 306;
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Publication No. US20030036176A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               2.3%;
ilarity 45.5%;
Conservative
                    WATANABE, HIDEMI
APPLICANT: SHIGENOBU, SHUJI
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                      ; ORGANISM: Buchnera
US-09-790-988-1
                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 640681
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Best Local Simi
Matches 260;
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US-09-927-827-35
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                                                                                                                                                                                                                                                                                                                                                                                                           88;
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/279,493
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 69
SEQ ID NO 35
LENGTH: 4880
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                                                                                                                                                                    TYPE: DNA ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (1001)..(3880)
US-09-927-827-35
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March 25, 2003, 18:27:39 ; Search time 381.22 Seconds
(without alignments)
14774.266 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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2501
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Gibberelllin-20-ox Arabidopsis thelia	Arabidopsis thalia	Gibberelllin-20-ox	Citrullus lanatus	Gibberelllin-20-ox	cDNA encoding a C-	Rice qibberellin 3 .	Sovbean C-20 oxida
SUMMARIES	AAQ75360 AAD16847	AAC42398	AAQ75361	AAD21991	AAQ75359	AAZ99483	AAH46556	AAZ99421
DB	16	21	16	24	16	21	22	21
% Query e Match Length DB I	1259	1169	1490	1420	1395	1161	1122	1077
% Query Match	11.7	11.6	10.8	6.5	9.1	9.1	7.0	6.1
Score	292.4	290.8	271	229.6	228	226.4	174	153.2
Result No.	1 7 7	ĸ	4	Ŋ	9	7	œ	6

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ppodental and and and and	Human colon cancer FigA insert stabil Rice gibberellin 3 Genomic clone GllF MiSP1-containing P Mheat flavonol syn Arabidopsis thalia Arabidopsis thalia Gibberelliin-20-ox RT-PCR product of Genomic sequence e Human adenosine Al Corn tassel-derive Human breast cell Human foetal liver	enic plant;
AAR29478 AAH46555 AAA146555 AAA55831 AAA52834 AAA75454 AAA75454 AAA72475 AAA23778 AAA23778 AAA222248 AAA222248 AAA55553 AAA55553 AAAA55553 AAAA56553 AAAA56553 AAAA56553 AAAA56553 AAAA56553	AAAOU2484 AAAAOU2484 AAAU55930 AAAQ55750 AAAQ59470 ABAC33593 AAXC4613 AAXC4614 AAXC4614 AAXC4614 AAXC491 ABAS0433 ABAS0433 ABAS8382	mRNA; 1259 BP. asmid pAt2301; transgenic ualifiers -20-oxidase" 4. 7. ATION.
8.1		d; cDNA to rst entry) oxidase. xidase; pla ; ss. lana. Location/Qu 12142 a /*tag= a /note= "GA 4WO-EP01664
	8 8 8 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	1 60 AQ75360 sta AQ75360, 1-JUL-1995 ibberelllin rop improve rabidopsis ey B-DEC-1994, 4-MAY-1994; B-MAY-1993; LONG-) LONG
		RESCULT AAOO 151 AAOO

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TICCICIGCCCGGAGAIGGACACGGIGCIGCCCCGCCGGAGGAGCIGGICGACGACCAC 1718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1259 BP; 368 A; 304 C; 246 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             growth rate; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200166777-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444 TCCACCAAGCTTCCATGGAAGGAGACCTTTCTTTCCGGT-----TTTGCGACGAC 494
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                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          clone pAt2301 containing DNA encoding gibberellin-20-oxidase may be used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterlum-mediated transfer.

Propagated transgenic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs reduces vegetative growth in cereals and grasses, improving resistance to frost, etc. Sense constructs improve fruit set and growth, extended stems and leaves, induce flowering and overcome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            495 ATGAGCCGCTCAAAATCCGTTCAAGATTACTTCTGCGATGCGTTGGGACATGCGTTTCAG
                                                                                                                                                                                                                                                                                              Preferred transgenic plants are maize and wheat.
                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                             DB 16; Length 1259;
                                              New DNA encoding gibberellin 20-oxidase and related vectors -
also host cells and transgenic plants, used to modulate plant
growth and development, e.g. anti:sense constructs will reduce
                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                              Sequence 1259 BP; 368 A; 304 C; 246 G; 341 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                           Score 292.4; DB 16;
Pred. No. 1.2e-48;
0; Mismatches 336;
                                                                                                                              Claim 9; Page 75-76; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                             ilarity 60.0%;
Conservative
1995-022813/03.
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Matches 532; Conserv
                                                                                                 regetative growth.
                 P-PSDB; AAR64143.
                                                                                                                                                                                                                                                                                              dormancy, etc.
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species plant belonging to the species Populus tremula x. Fremulations exhibiting at least one improved growth parameter, in that a DNA sequence coding for expression of a polypeptide exhibiting plant hormone gibberlin (GA) 20-oxidase activity functionally inserted in the plant industries. The transgenic plant has increased growth rate, biomass production and/or xylem fiber length. The ectopic overexpression of GA 20-oxidase gene results in significant changes in growth rate, stem $20-oxidase gene results in significant changes in growth rate, stem growth influencing chemicals in forestry. The present sequence is Arabidopsis thaliana gibberellin (GA) 20-oxidase cDNA construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a transgenic woody plant e.g. a Populus
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CACCCGAGGGTGTACCCGGACTTCACGTGGCGGGCGCTGCTGGACTTCACGCAGCGCCAC 1778
                                                                                                                                           Transgenic plant, plant hormone, gibberellin; GA 20-oxidase, forest, pulp; paper industry; biomass production; xylem fibre length;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Arabidopsis thaliana gibberellin (GA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana gibberellin (GA) 20-oxidase cDNA construct.
                                                                                                                                                                                                                                                                            1779 TACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTA 1824
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12..1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD16847 standard; cDNA; 1259 BP
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/product= "A:
20-oxidase"
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13-0CT-2000; 2000US-0240319.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
         Arabidopsis thaliana DNA fragment SEQ ID NO: 35404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0138540.
99US-0138847.
99US-0139119.
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                                                                              Arabidopsis thaliana
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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                                                        939 GAGGCGTGCGAGGCACGCCTTCTTCTTGCTGGTTAACCACGGCATCGAGGCGGCGCTC 998
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                                 18;
           DB 22; Length 1259;
         Score 292.4; DB 22; Length
Pred. No. 1.2e-48;
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- JUN-1999; - JUN-1999; - JUN-1999; - JUN-1999; - JUN-1999; - JUN-1999;	0-JUN-1999; 1-JUL-1999; 1-JUL-1999; 2-JUL-1999; 5-JUL-1999; 3-JUL-1999;		70L - 1999; 70L - 1999;	2-70L-1999; 2-70L-1999; 3-70L-1999; 3-70L-1999; 5-70L-1999; 7-70L-1999; 7-70L-1999; 8-70L-1999; 8-70L-1999;	2-AuG-1999; 2-AuG-1999; 3-AuG-1999; 4-AuG-1999; 4-AuG-1999; 5-AuG-1999; 6-AuG-1999; 6-AuG-1999; 6-AuG-1999; 9-AuG-1999; 9-AuG-1999; 9-AuG-1999; 9-AuG-1999; 9-AuG-1999; 9-AuG-1999;	AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999;
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Pred. No. 2.4e-48;
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                                                                                                                                                                                                                                                                                                                    Clone pAT2353 containing DNA encoding gibberellin-20-oxidase may be used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterium-mediated transfer. Propagated transgenic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 AAGACTATIGIGAAGCAATGAGTICTCTATCACTCAAGATCAGGAGCTICAGGGCTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCCAAGACTCGACTCTTGAAGCTCCTAGAGTCATCGCAGAAGCTTGCACCAAACACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reduces vegetative growth in cereals and grasses, improving resistance to frost, etc. Sense constructs improve fruit set and growth, extended stems and leaves, induce flowering and overcome dormancy, etc. Preferred transgemic plants are maize and wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                            New DNA encoding gibberellin 20-oxidase and related vectors -
also host cells and transgenic plants, used to modulate plant
growth and development, e.g. anti:sense constructs will reduce
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Pred. No. 2.2e-44;
                                                                                                                                                                                                                                                             Claim 10; Page 78-79; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.8%;
Best Local Similarity 56.5%;
Matches 593; Conservative
WPI; 1995-022813/03.
P-PSDB; AAR64144.
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                                                    CGGICGICAACAGCACGCGCCCCCCCCCCCGCTGCCTTCTTCCTCCTCCGGGAATGG 1677
                                                                                                                                                                               1114 ACTICACTIGGICTATGITCCTIGAGITCACTCAAAAACATTACCGAGCAGATGIGAATA 1173
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GACCICATIGIGATCCAAGIICTTIGACCATCCTTCAICAAGACCAIGICAATGGCCTTC 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to testa specific Cv20ox gene, a gibberellin 20-oxidase (GA 20-oxidase) gene which is integument-specifically expressed in seeds of the Citrullus lanatus, and proteins encoded by such genes. The invention also relates to Cv20ox promoter
                            Testa specific Cv20ox gene; gibberellin 20-oxidase; GA 20-oxidase;
Cv20ox promoter; Cv20oxP; seedless fruit generation; watermelon;
melon; ss.
                                                              Novel testa specific Cv20ox gene, a gibberellin 20-oxidase is integument-specifically expressed in seeds of Citrullus useful for producing seedless fruits such as melon
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(Cv20oxP) which regulate the expression of Cv20ox gene and method for generating seedless fruits of gourd family such as melon or watermelon using the Cv20ox sequence. The present sequence is C. lanatus Cv20ox cDNA coding for GA 20-oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 IGAIGIGAAACAAAAICICAAAGGAAATIIGGIGAAAITAIGGGIAIGCIAAIAGCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTGGAAGATTCTCCAATAATCTTCCATGGAAGGAAACCCTTTCCCTTC-----
                                                                                                                                                                                                 DB 24; Length 1420;
                                                                                                                                         Sequence 1420 BP; 412 A; 257 C; 329 G; 422 T; 0 other;
                                                                                                                                                                                                                        .7e-36;
es 384;
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                                                                                                                                                                                           9.2%; Score 229.6;
55.3%; Pred. No. 3.7e
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nes 501; Conserv
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1588 ACGCCAGGTACCGCAGCTGCCTGCACCGGCCGGTCGTCAACAGCACGGCGCCTCGCCGCT 1647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1768 OGCAGCGCCACTACAGGGCCGACATGCGCACGTTCAGGCCTTCTCCGACTGGCTTAA 1825
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                                                                                                                                                                            646 ACTICAAGAATTICITCGAGGACAACGATTCAATATTGAGGCTTAATTACTACCAACAT
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                                                                                                                                                                                                                                                                                         ACTICCGGCGATICTICCAGCGCAACGACTCATCATGCGCCTCAACTACTACCCGGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a C-20 oxidase polypeptide.
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/product= "C-20 oxidase"
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1..1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vectors containing DNA encoding gibberellin-20-oxidase activity are used to construct chimeric genes and binary vectors to transform plants by usual methods, e.g. Agrobacterium-mediated transferm. Propagated transgemic plants show modulated growth and development e.g. reducing GA-20-oxidase expression with antisense constructs reduces vegetative growth in cereals and grasses, improval resistance to first, etc. Sense constructs improve fruit set and growth, extended stems and leaves, induce flowering and overcome dormancy, etc. Preferred transgemic plants are maize and wheat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAGGTGGGGAAGGCGTGCGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding gibberellin 20-oxidase and related vectors - also host cells and transgenic plants, used to modulate plant growth and development, e.g. anti:sense constructs will reduce vegetative growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1395;
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                                                                                                                                                                                                                                        Gibberellin-20-oxidase; plasmid pB11; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 1395 BP; 404 A; 288 C; 336 G; 367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           380;
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Pred. No. 7.6e-36;
0; Mismatches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phillips A;
                                                                                             BP
                                                                                                                                                                                                                                                                                                                                               15..1341
/*tag= a
/note= "GA-20-oxidase"
                                                                                         AAQ75359 standard; cDNA to mRNA; 1395
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Best Local Similarity 55.3
Matches 497; Conservative
                                                                                                                                                                                                    Gibberelllin-20-oxidase
                                                                                                                                                                                                                                                              crop improvement; ss.
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P-PSDB; AAR67450.
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 1167 AAAACA 1172
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                                                                                                                              AAQ75359;
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GCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCA 1467
    632 ACTICAAGAAITTCTICGAGGACAACGATTCAATATTGAGGCTTAATTACTACCCAACAT 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES (RIKE ) RIKEN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuoka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rice gibberellin 3beta-hydroxylase cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 53-56; 68pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       new breeds of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-418072/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200146434-Al
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                                                                                                                                                                                                                                                                                                                                                             a chimeric expression construct expressing a RNA or protein which suppresses the gibberallin biosynthetic pathway sequence, divarts substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, 3beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to requilate gene products of gibberallin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberallin deficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1227
                                                                                                                                                                                                                    Obtaining transgenic plant useful for controlling seed germination and seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 GGGAGAAGCAGCGGGCGCAGCGCGCGCGGGGAGAGCTGCGGGCTACGCCAGCAGCTTCA 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1288 CGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGGAGACCGGCGCCACT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTICCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTACTACCCGGCGT 1407
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                                                                                                                                    SJ;
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                                                                                                                                                                                                                                                                                                                       is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be inhibited or controlled by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GGCTGGTGGATGAGGCTTGTAGACAACATGGCATATTTTTTGTGGGAACCATGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             928 GGCAGGTGGGGGGGGGGGGGGAGGCCACGGCTTCTTCCTGGTGGTTAACCACGGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 ATCTGAAGCAGAGGCTAAGAGGAAGGTAGGTGAGGTTATGGATATACCAATAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1108 CGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 TIGGGAGALICGCGICCAAICTICCAIGGAAGGAAACCITITCCCITCGCTGTGTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1168 CTGGAGATGAAGAGGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 CTCAAAACTCCTCCGCGCCTCATGACTATGTTCTTGACACTTTAGGCCCCATCATTCTCCC
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                                                                                                                                  Logusch
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                                                                                                                                                                                                                                                                                                      The present sequence encodes a C-20 oxidase polypeptide, which
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                                                                                                                                 Logusch EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1161 BP; 307 A; 251 C; 303 G; 300 T; 0 other;
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                                                                                                                                 Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 226.4;
                                                                                                                                                                                                                                                                           Claim 45; Page 257; 267pp; English.
                                                                                                                               Heck GR,
                                                                                                                                                Ream JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%;
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99US-0137977
                              99WO-US18066
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                                                                                                                               Elich TD,
                                                                                                                                                                          WPI; 2000-224351/19.
                                                                                                    (MONS ) MONSANTO CO.
                                                                                                                                                Rao S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                         P-PSDB; AAX84102
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                            10-AUG-1999;
                                                         10-AUG-1998;
07-JUN-1999;
24-FEB-2000
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                                                                                                                                 SM,
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Rice, gibberellin 3beta-hydroxylase, growth inhibition, gene expression, crop yield; plant breeding; plant regeneration; growth control; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNAs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth or to improve crop yield and management. They are useful for producing
                                                                                                                                                                                                                                                                       1587
                                                                                         1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1588 ACGCCAGGTACCGCAGCTGCCTGCACCGGCGGTCGTCAACAGCACGGCGCCTCCGCCGCT 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      992 TGGAGAAGAGTCCACCACGAAAGTATCCAGATTATAAATGGCCAATGTTGCTTGAAATGA 1051
                                                                                                                                                                                                                                                                                                                                                            871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1052 CCCARARGCGTTACCGACCTGATTGCAACACTTTGGAAGCCTTCAAAACTTGGGTTCA 1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATTGGCCTTCTTCTGTCTGTCCATCGCATGACAAGTGGTGAGAGCACCGGAGGAATTGG
                                                                                         TOCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGGAGGGGCGGTGGCGCGCCC
                                                                                                                                                                         TCCTTCACCAAGACCCTGTCAGTGGCCTTCAAGTGTGCTCCAATGATCAATGGTATTCAA
                                                                                                                                                                                                                                                                                                                                                            812 TICCICCAAACCCAGAAGCCTTTGTCATCAACATCGGTGACACTTTCACGTCTCTCACGA
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new breeds of plants, for producing a higher harvest of feeding materia for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the gene, expression. The present sequence encodes a rice gibberellin 3beta-hydroxylase enzyme of the invention.
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                                                                                                                                                            18;
                                                                                                                            Length 1122;
                                                                                                                                                            Indels
                                                                                             Sequence 1122 BP; 137 A; 406 C; 410 G; 169 T; 0 other;
                                                                                                                           Score 174; DB 22;
Pred. No. 3.9e-25;
0; Mismatches 495;
                                                                                                                         7.0%;
                                                                                                                           Query Match 7.0
Best Local Similarity 49.8
Matches 509; Conservative
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The present sequence represents the C-20 oxidase polynucleotide sequence is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels. Gibberellic acid levels may be control of gibberellic acid levels. Gibberellic acid levels may be controlled by use of a chimeric expression construct expression and a Protein which suppresses the gibberellin construct chorythetic pathway sequence, diverts substrate from the pathway, or degrades pathway substrates or products. The methods uses copally diphosphate synthase, Bata-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, 3beta-hydroxylase polynucleotides to achieve this. The method is used to control seed germination and seedling growth especially to regulate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin deficient, and have
                                                                                       995 AGTACATGGCCGTCCGCAAGAAGGCCTTCGCCACGGCGGCTCCGCCCTCAAGATGGTCT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Obtaining transgenic plant useful for controlling seed germination an seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
                                                                                                                                                                                                                                                                                                                                                                                      Gibberellič acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytoene synthase; C-CO oxidase; 2beta, 3beta-hydroxylase; seed germination; seedling growth; gibberellin biosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
CGCIGCIGGACTICACGCAGGCCCACIACAGGCCGACAIGCGCACGCTICAGGCCTICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 153.2; DB 21; Length 1077; Pred. No. 5.2e-21; 1; Mismatches 450; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hortened hypocotyl and/or epicotyl phenotypes compared to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĒΜ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1077 BP; 316 A; 219 C; 248 G; 288 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Logusch
                                                                                                                                                                                                                                                                                                                                                        Soybean C-20 oxidase polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 45; Page 227-228; 267pp; English.
                                                                                                                                                                                                                                                  BP
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                                                                                                                                                                                                                                                  AAZ99421 standard; DNA; 1077
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07-JUN-1999;
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                                                                                                                                                            246 AGCAGAGCTIGIGAGAAAAGCAIGCTIGAAGCAITITICCAAGTGAIAAACCAIGG 305
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                                126 GCCCAAAGAGTICCTTIGGCCTTCTAGGGACTTGGTTGACACCACCCAAGAGGAGCTAAA 185
                                                                                                                                      923 GGTCCGGCAGGIGGGGAGGCGIGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGG 982
                                                                                                                                                                                                                                 ATTTATCTTTAGTAATTATGGAGCTATTGGTRTATTWGKTTG------GGTGTGGATC
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                                                                   -----TGATCACCAAAGCTTCTCCAACTCCCAGATTGTTGACTACTTCAAGTCTGTGT
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The present sequence represent a gibberellic acid 2-oxidase 2 cDNA sequence, which is used in the method of the invention. The specification describes methods for the inhibition and control of gibberellic acid levels may be inhibited or controlled by use of a chimeric expression construct expressing a RNA or protein which suppresses the gibberellin biosynthesic pathway sequence, diverts to substrate from the pathway, or degrades pathway substrates or products. The methods uses copalyl diphosphate synthase, and a 2beta, Beta-hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta, Beta-hydroxylase polyuucleotides to achieve this. The method is used to control seed germination and seedling growth especially to requilate gene products of gibberellin biosynthetic pathway and restoration of normal seed germination, in transgenic plants. The plants produced are gibberellin ceficient, and have shortened hypocotyl and/or epicotyl phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1274 GATGAGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGG 1333
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                                                                                                                                                                                                                                                                                                                                                                                                     Logusch SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obtaining transgenic plant useful for controlling seed germination an seedling growth comprises transgene comprising a sequence expressing altered levels of an essential hormone.
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                                                   Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase; 2-oxidase; phytocone synthase; C-0 oxidase; 2beta,3beta-hydroxylase; seed germination; seedling growth; gibberellin blosynthetic pathway; transgenic plant; hypocotyl; epicotyl; ss.
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                 Maize gibberellic acid 2-oxidase 2 cDNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                   Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 45; Page 253; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   GR,
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Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                             (MONS ) MONSANTO CO.
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GGACGCCGCTGGGCCTCCGTCCGCCCGACGGGGACGCCTTCTTCGTCAACGTCGGCGA 321

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(first entry)

03-JUL-2000 AAZ99478;

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12-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNAs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth or to improve crop yield and management. They are useful for producing new breeds of plants, for producing a higher harvest of feeding materials for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the gene expression. The present sequence is genomic DNA encoding a gibberellin 3beta-hydroxylase enzyme.
                                                                                                                                                                                                                                                                                                    Rice, gibberellin 3beta-hydroxylase, growth inhibition, gene expression, crop yield, plant breeding; plant regeneration; growth control; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice-originated gibberellin 3approximatelyb-hydroxylase and encoded agenes for regulating gibberellin activation e.g. to inhibit elongative growth or to improve crop yield and management, applicable to produce new breeds of plants
                                                                                             GCGCCCGCCGGAGGAGCTGGTCGACCACCACCACCAGGGGTGTACCCGGACTTCACGTG 1747
         CAGCACGGCGCCTCGCCTCGCTGGCCTTCTTCCTCTCCCCGGAGATGGACACGGTGGT 1687
                             381
                                                                322 CACCCTGCAGGTGTTGACGAGGTTCAGGAGGGTGAGGCAGGGTGGTGGTGAA
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                                                                                                                                                                                                                                                                                Rice gibberellin 3beta-hydroxylase genomic DNA #2.
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(RIKE ) RIKEN KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 60-63; 68pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                AAH46558 standard; DNA; 2112 BP.
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                                                                                                                                                                                                                                                                                               1328 CGTCGGAGACCGGCGCCCACTACTTC-----CGGCGATTCTTCCAGCGCAACGACTC 1378
                                                                                                                                                                                                                                                                                                                                                   981 CACCGGCGAGGAGGTCGCGGAGTCGAGGCGGAGGATCGGCGAGGAGGATGACGGC 1040
                                                                                                                                                                                                                                                                                                                                                                                                             1379 CATCATGCGCCTCCAACTACTACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGG 1438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 CGCGCACACGGGCTTCTTCACCTTCGTGCTCCAGAGCCTCGTCCGGGGGCTGCA 1160
                                                                                                                                                                                 1268 CCACGAGATGAGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCAT 1327
                                                                                                                                                                                                                                        921 CAAGGAGATGCGGCGCCTAGCCGACGAGTTGCTGAGGTTGTTCTTGAGGGCGCTGGGGCT 980
                                                                                                                       Gaps
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                                                                DB 22; Length 2112;
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Sequence 2112 BP; 462 A; 585 C; 576 G; 489 T; 0 other;
                                                          Score 126.4; DB 22;
Pred. No. 1.3e-15;
0; Mismatches 241;
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(RIKE ) RIKEN KK.
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                                                             Query Match 5.1%;
Best Local Similarity 54.4%;
Matches 306; Conservative
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1449 GACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV55831 standard;
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15-NOV-1996;
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                                                                                                                                                                                                                                                                      or to improve crop yield and management. They are useful for producing new breeds of plants, for producing a higher harvest of feeding materials for animals and in plant regeneration. They are used to control the growth, size and shape of plants, e.g. dwarf plants, by inhibiting the spene expression. The present sequence encodes a rice gibberellin 3beta-hydroxylase enzyme of the invention.
                                                                                Rice-originated gibberellin Sapproximatelyb-hydroxylase and encoded genes for regulating gibberellin activation e.g. to inhibit elongative growth or to improve crop yield and management, applicable to produce
                                                                                                                                                                                                  The invention relates to nucleic acid molecules from Oryza sativa that encode proteins with gibberellin 3beta-hydroxylase activity. The protein, the genes that encode them and antisense DNAs are useful for regulating gibberellin activation, e.g. to inhibit elongative growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        969 GTGGTTAACCACGGCATCGAGGCGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCC 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1209 GTGCGGAAGCTCGGGGCGGAGCACGGCGGCGGCTGGGCGAGGTGTACTCGCGCTACTGC 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGGAGACCGGCGCCACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGC 1388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              789 GCGGTGCTGAGCGGCAGACGGAGATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGAGC 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     909 GAGAGGTCGTCGGTCCGGCAGGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 ACCGCTACGCCGCCGCCGCACCTCCTCCGGTACCCGAAGCAGATGTGGGGCCGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445 TACACCTTCCCTCCCCTGCCATCCGCGACGAGTTCCGCCGCGCTCTGGCCCGACGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 GACGACTACCACCGCTTCTGCTCCGCCATGAGGGGAGGAGCACGACGACGATGAGAGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1269 CACGAGATGACCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     565 GCCGAGAGGCTCCTCGCCATGTTCTTCAAGGCGCTCGGGCTCGCCGGCAACGATGCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        625 GGCGGCGAGCGGAAGATCCGCGAAACGTTGACGTC-----GTCGACGATTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 1187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1187 BP; 202 A; 378 C; 424 G; 183 T; 0 other;
 Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 532;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 114.8; DB 2
Pred. No. 2.3e-13;
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Matsuoka
                                                                                                                                                                Claim 1; Page 49-52; 68pp; Japanese.
Yano M,
                                                                                                                                                                                                                                                                                                                                                                                                                              4.68;
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                                                                                                                                    new breeds of plants
                                2001-418072/44
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
Kayano
                                                  P-PSDB; AAG64062
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Fusion protein; stabilising polypeptide; proteolytic degradation; resistance; half-life; autolimune disease; inflammation; intro drug; IkappaB requlator protein; inflammatory bowel disease; in vivo imaging; nitroreductase protein; enzyme therapy; prodrug therapy; protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GICAACAGCACGGGGCCTCGCTGGCTGGCCTTCTTCTTGCCCGGAGATGGACACG 1682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          978
                                                                                                                                                                                        858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion proteins resistant to proteclytic degradation - comprising a core protein with a stabilising polypeptide comprising a peptide sequence containing glycine repeats
                                                                                                                                                                                                                                                                                                                919 GIGAACCGGGGGAGAGACGCCGGATCICCTTCCTCGGTCCGCCGGCCGACGTG
1503 TGGGCGGAGGGGCGGTGGCGCCCATCCGCCCTCGCCCCGGGGGCGCTCGTCGTCAACGTC
                                                                                                                                                                                        799 CACCGGCCGGACCGTGACGCTTCCGGGGACGCCGGGGGGCCCTCATCGTCGTCGTC
                                                                                                                                                                                                                                                                              1683 GTGGTGCGCCCGCCGGAGGAGCTGGTCGACGACCACCACCGGAGGGTGTACCCGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the stabilising sequence-encoding insert.
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11-FEB-2000; 2000WO-US03547

(PHAR-) PHARMACOPEIA INC

11-FEB-1999;

Chelsky

Horlick RA,

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encoding the stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the unfused core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroeductase protein which can activate nitro drugs in eargue/prodrug therapy to treat cancer our other pathological conditions. The fusion proteins can also be used in diagnostic methods such as In vivo imaging.
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                                                                                                                                                                                                                                                                                   752 GGTGGTGCAGCAGGAGCAGGAGGTGGTGTTCGACGCGGCGGTGCTGAGCGGCCAGACGGA
                                                                                                                                                                                                                                                                                                                 GAICCOGICGCAGIICATAIGGCCGCGGAGGAGAGCCCCGGGICGGIGGCGGIGGAGGA
                                                                                                                                                                                                                                                                                                                                            GCTGGAGGTGGCGCTGATCGACGTGGGGGCGGGGGCGGAGAGGTCGTCGGTGGTCCGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear antigen 1; EBNA1; episome; transfection; selection;
                                                                                                                                                                                                                              ó;
                                                                                                                                                                                             Score 94.4; DB 19; Length 799;
Pred. No. 2.3e-09;
0; Mismatches 256; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA
                                                                                                                                                                   Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1232 CGGGGGGGCGCTGGGCGAGGTGTA 1255
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                                                                                                                                                                                             3.8%;
ilarity 49.2%;
Conservative (
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                                                                                                                                                                                                             Local Similarity
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The present sequence is that of DNA encoding the Epstein-Barx virus (EBNA) nuclear antigen protein 1 (EBNA), see AAY95856). EBNA1 is utilised in a novel method for obtaining a eukaryotic cell that is stably transfected with a least one episome. This method involves transfecting a eukaryotic cell with: (1) a first episome comprising an EBV origin of replication (oriP, see AAA5025), a gene encoding a first protein whose expression results in cell death and a selectable marker for eukaryotic cells; and (2) a second episome comprising an EBV oriP and a gene encoding a second protein, where comprising an EBV oriP and a gene encoding a second protein prohibits the occurrence of cell death resulting from expression of the first protein to produce doubly transfected cells which also express an antigen that promotes retention of the episomes by the cells. The doubly transfected cells are maintained under conditions in which the first and second proteins and the selectable marker is maintained. Under these conditions, only cells containing both episomes live. Preferably, EBNA1 is expressed from 1 of the episomes, and the protein of interest from the other episome. Either or both
                                                                                                                                                                                                                                                 Stably transfecting eukaryotic cells with at least one episome for the production of a desired protein in vitro and for gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1052 GAAGCAGCGGGCGCAGCGGCGCGGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGG 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       992 GCCGCTGCTGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGA 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              932 GGTGGGGGGGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGCCATCGAGGC 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 872 GCTGGAGGTGGCGCTGATCGACGTGGGGGCGGGCGGAGAGGTCGTCGGTGGTCCGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein may further comprise a nucleic acid sequence encoding a protein desired to be expressed in the cell (e.g. a therapeutic protein), a nucleic acid encoding an RNA that is not intended to be translated (e.g. a therapeutic RNA), or a DNA sequence used as a tag for the cells. The method is applicable to cell culture or intact organisms, for gene therapy. It allows the rapid
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Pred. No. 2.9e-09;
0; Mismatches 256; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selection factors, such as antibiotics.
                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 2; 53pp; English.
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                                                                                                                                                                                                      P-PSDB; AAY95856
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protein and expression vector operationally encoding a protein sultable for tethering the nucleic acid to the histome HI protein, where the rethering protein is LANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to Histome HI. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histome HI and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis. Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Epstein-barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides a composition comprising nucleic acid, histone H1
                                                                                                                                                                                                                                                                                                                                                                                                                Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis; Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8; EBV; latency-associated nuclear antigen; LANA; EBNA1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A composition for use in gene therapy comprises an expression vector that includes a nucleic acid sequence encoding a nucleic acid binding
                                                 1112 GCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGC 1171
                                                                                                            1172 AGAIGAAGAGGCGAGGAGGGCGIGGGIGAGIACCIGGIGCGGAAGCICGGGGCGGAGCA 1231
                   699
                                                                                                                                EBV tethering protein EBNAl encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1926
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                                                                                                                                                                             CGGGCGCGCTGGGCGAGGTGTA 1255
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P-PSDB; AAB62332.
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Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;

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 Length 1926;
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3.8%; Score 94.4; DB 22;
49.2%; Pred. No. 2.9e-09;
tive 0; Mismatches 256;
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BG4141208 HVSMEC000
BB454826 HVSMEC006
BB422495 WHE0056_E
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1 (bases 1 to 1435)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
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Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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BG365195 HYSKE1000
BG365194 HYSKE1000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                          /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed buront contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               984 AICGAGGCGCCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCG 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIGGGGGAGAAGCAGCGGGGGGGGGGGGGGGGGAGAGCTGCGGCTACGCCAGCAGC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1104 ITCACGGGGGCGTTCGCGTCCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCA 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1164 TCGCTGGAGATGAAGAGGGCGAGGAGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGG 1223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTACTTCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTACTCCCG 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1404 GCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGCACTGCGACCCCACCTCGCTC 1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1464 ACCATCCTCCACCACGACCACGTCGGCGGCCTGGAGGTGT-----GGGCGGAGGGGCGG 1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1518 TGGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCAACGTCGGCGACACCTTCATG 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGCTCTCCAACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCG 1637
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                                                                                                                                                                                                                                                      67 AIGGIGCIGCCIACGAICCCCCITCCCCTIGIGTTCGACGCTGCCCGCCTGAGCGGC 126
                                                                                                                                                                                                                                                                                    CAGACGGAGATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGACCCCGGGTCGGTGGCC 863
                                                                                                                                                                                                                                                                                                                 CTCTCCGACATCCCGCAGCAGTTCATCTGGCCGGCGGACGAGGCCCCACCCCGGACTCC 186
                                                                                                                                                                                               Gaps
/clone_lib="Maize Mapping Project/DuPont Cornsensus
                                                                                                                                                                                                                                                                                                                                            GICCGGCAGGIGGGGAGGCGIGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 ATCGACGCGCTGACGCCGGAGGCCCACCGCTGCATGGACGCCTTCTTCACGCTGCCGC
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                                                                                                                                                                Score 629.4; DB 11; Length 1435;
                                                                                                                                                                                               Indels
                                                                                                                                                                              Pred. No. 1.1e-118;
0; Mismatches 241;
                                                                                                                     263 t
                                                                                                                    427 g
                                                                                                                                                                25.2%;
75.9%;
                                                                                                                     461 c
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                 Library
                                                                                                                                                                              Similarity
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Local Sr.
825; C
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1. .536
/organism="Sorghum bicolor"
/do_xref="taxon:4558"
/clone_lib="Embryo 1 (EM1)"
/olone_loggan: Embryos germinated for 24 hr; Vector:
pBluescript II from Lambda Zap II; Site_l: XhoI; Site_2:
BCORI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG322884 536 bp mRNA linear EST 27-FEB-2001 EM_15_C10.bl_A002 Embryo 1 (EM1) Sorghum bicolor CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences have been trimmed to exclude PolyA, vector and regions.
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                  1071
                                                       952 GCACGCCCCTCGCTCCTTCTTCCTGTGCCCGGAGATGGACAAGGTGGTCAGGCCGCCC 1011
                                                                                                                                                                        GAGGAGCTGGTCGACGACCACCCGAGGGTGTACCCGGACTTCACGTGGCGGGGGGTG 1757
                                                                                                                                                                                                                                                                                      CIGGACTICACGCACCACTACAGGCCGACAIGCGCACGCTICAGGCCTICTCCGAC 1817
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892 GCGCTCTCCAACGGGCGCTACAGGAGCTGCCTCCACCGCGCCGTCGTCAACAGCCGGGTG 951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                          9 AGCAGCTTCACGGGCCGCTTCGCGTCCAAGCTGCCATGGAAGGAGGAGCTGCTGGTCGTTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1072 CTGGACTTCACCATGAGGCACTACAGGTCGGACATGAGGACGCTCGAGGCCTTCTCCCAAC
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76.6%; Pred. No. 1.8e-48;
ive 0; Mismatches 92
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POLYA=No.
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Sequences have been tri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 706 542 1860
Fax: 706 583 0210
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1394 CTACTACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCC 1453
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1 (Dases 1 to 755)
Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 20 DAP spike cDNA library Unpublished (2001)
On Mar 8, 2001 this sequence version replaced gi:13254292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVSME10001L04f Hordeum vulgare 20 DAP spike EST library HYCDNA0010 (20 DAP) Hordeum vulgare CDNA clone HVSME10001L04f, mRNA sequence. BG365195.2 GI:16323591
                                                                                                                                                                                                                                                                                                                                                                                                                                ------AGGGGCGGTGGCGCGCCCATCCGCCCCGGGGGGGCGCTCGTCGTCAAC 1559
                                                                                                                                             1338 CGGCGCCACTACITCCGGCGATTCTTCCAGCGCAACGACTCCATCATGCGCCTCAACTAC 1397
                                                                                                                                                                                                                   TACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACC 1457
                                                                                                                                                                                                                                                                                        TCGCTCACCAICCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGG----- 1509
1218 CTCGGGGGGGAGCACGGGCGGCGGCTGGCGAGGTGTACTCGCGCTACTGCCACGAGATG 1277
                                                                        AGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGAGAGCCTGGGCATCGTCGGAGAC 1337
                                                                                                                                                                 -GCCGCCGCCACTICCGCCGCTTCCTAGGGGAACGACTCCATCATGCGCCTCAACTAC 290
                          /db.ref="laxon:4513"
/clone="HVSME10001104f"
/clone_lib="Hordeum vulgare 20 DAP spike EST library
HVcDNA0010 (20 DAP)"
                                                                                                                                                                                                                                                                                                                      351 TCCTCACCATCTCCACCAGGACGACGAGGACGCCTCCAGGTGTTCGACGCCGCCACC
                                                                                              411 GGCCCCGCACCGGCCGCTCCATCAGGCCCCACCGGGCGCCCTTCGTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
100 Uordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
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Seq primer: AATTAACCCTCACTAAAGGG
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High quality sequence stop: 6
Location/Qualifiers
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Hordeum vulgare
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BG365195
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From the form of the feature of the 
                                                                                                   /note="Vector: lambda2AP; Site_1: EcoR1; Site_2: Xhol; Plants were grown in the greenhouse at the University of California. Riverside (Fenton, S7 Close, TJ Close). Whole spikes with awns trimmed were collected at 20 pap (Fenton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
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Pred. No. 1.4e-46;
0; Mismatches 231;
'tissue_type="20 DAP spike'
                                                               /lab_host="SOLR"
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65.4%;
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
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                                                                                                                                                                                                                22;
                                                                                                                                                       Score 263.4; DB 12; Length 752;
Pred. No. 1e-43;
0; Mismatches 221; Indels 22;
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Ana_Luber_Solura

Plants were grown in the greenhouse at the University of

Plants were grown in the greenhouse at the University of

Callfornia, Riverside (Fenton, SJ Close, TJ Close). Whole

spikes with awns trimmed were collected at 20 DaP (Fenton

). Total RNA was prepared, Poly(A) RNA was purified, one

primary unamplified cDNA library was made, and I million

pit were in vivo excised to give paluescript SK(-) cDNA

phagemids in the TJ Close lab at the University of

Callfornia, Riverside (Choi). Phagemids were plated and

picked at the Clemson University Genomics Institute (CUGI)

(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA

preparations, DNA sequencing and sequence analysis were

performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates,

'Rambo, Main). The sequence has been trimmed to remove

vector sequence and contains a minimum of 100 bases of

phred value 20 or above. For more details on library

preparation and sequence analysis sec
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Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu. Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton Y., Berry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton Development of a genefically and physically anchored EST resource for barley genomics: Morex 20 DAP spike cDNA library Unpublished (2001)
On Mar 8, 2001 this sequence version replaced gi:13254291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                     752 bp mRNA linear EST 22-OCT-2001 HVSME10001L03f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10001L03f, mRNA sequence. BG365194
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                                                                              CACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCTGGAGGTGTGGGCGGAGGG 1513
                      583 CCACTACGCGCCATGCAATAAGCCTCACCTGACGCTGGGCCACGGGCCCGGACCACGACCC 642
                                                                                                                                 /clone="HVSWEI0001L03f"
/clone_lib="HOrdeum vulgare 20 DAP spike EST library
HVcDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
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/cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 586.
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Email: rwing@clemson.edu
Total hg bases = 558
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SOURCE

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918 TC--GGTGGTCCGGCAGGTGGGGAGGCGTGCGAGGCCACGCCTTCTTCCTGGTGGTTA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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/cultivar≈"Morex"
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Total hq bases = 162
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Fax: 864 656 4293
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Hordeum vulgare
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BE194605
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1 (bases 1 to 796)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W., Fenton, R.D., and Main, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for
                                                                                               resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="HYSMEa0020B13f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HYcDNA0001 (Cold stress)"
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/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
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for barley genomics: Morex cold-stressed seedling shoot cDNA
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68.6%; Pred. No. 2.6e-43;
Live 0; Mismatches 159; Indels
                                                                                                                                                                                  Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tael: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare"
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High quality sequence stop: 644.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Total hq bases = 587
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Tritcaee; Mordeum.

1 (bases 1 to 577)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,Y.D., R.D., Close,S.J., Oattes,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike CDNA library
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/clone_lib="HOrdeum vulgare 5-45 DAP spike EST library
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On Jun 26, 2000 this sequence version replaced gi:13187496.
Contact: Wing RA
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523 GAGGTGTTCACCGGCGCGCGCGTGGCGTGCCGTGCGGGCCCCGAGCGACGCTTCG 577
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                                                              Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Clase, TW Close). Whole spikes with awas trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Fotal RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(a) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give palbuescript SK(-) DNA phagemids (Chol)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clamfornia, Riverside. Phagemids were plated and picked at the clemson University Genomics Institute (CUGI) (Psgum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, YY, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or accommence analysis seen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genome.clemson.edu/projects/barley. To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGTTCTTCCAGGTCGTGAACCAGGCGTGGACCCGGCGCTGCTCGCCAAGGCGTACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 255.4; DB 10; Length 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.7e-42;
0; Mismatches 171; Indels
HVCDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.2%;
68.2%;
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Matches 406; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Seeds were surfaces sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly (A) RNA was purpared, poly (A) RNA was purified, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemon Divisity was made pricked at the Clemon Divisity of California, plane, Palmer, Filsch, Akkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                 EST 22-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Lillopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (Dases I to 914)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library On Dec 18, 2000 this sequence version replaced gi:11884239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/coders Also
see Close TJ, Wing R, Kleinhoffs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
306 c 279 g 198 f
brbzUbu5
HVSMEC0020B13f Hordeum vulgare seedling shoot EST library
HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEC0020B13f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Pax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="HVSMEc0020B13f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Total hq bases = 464
                                                                                                                                                                                                                        BF620505.2 GI:13109508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                           Hordeum vulgare.
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strain changes maintained in continuous 1251 of 1200, and 1200 of 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Whing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 205 / 184 g 138 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1411 AGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCATCC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1531 GCCCTCGCCCCGGGGCGCTCGTCGTCACGTCGGCGACACCTTCATGGCGCTCTCCAACG 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1591 CCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCGCTCGC 1650
                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1471 TCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGCGGAGGGGCGGTGGCGCGCATCC 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1711 AC---GACCACCACCGAGGGTGTACCCGGACTTCACGTGGCGGGGGGCTGCTGGACTTCA 1767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GGCCCCGGAGGCGTTCGTCGTCAACATCGGCGACACCTTCTCCGGGCTCACCAACG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 CCATTGATGGACGCCCGCGCGCGTGTACCCAGACTTCACTTGGCGTGAGTTCCTCGAGTTCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AGAAGCCTCACCTGACGCTGGGCACGGCCCGCACCACCACGGCGCTGACGCTGC
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Pred. No. 2.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="testa/pericarp"
/lab_host="TJC121"
                                                                                                                                                                                                                            /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
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   Email: rwing@clemson.edu
Total hq bases = 618
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              /clone="HVSMEk0013M18f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%;
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Best Local Similarity
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                                                                                                                                                                                                source
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ORIGIN
                                                                                                                                                     FEATURES
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Triticeae; Hordeum.

To Chases 1 to 682;

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von Wetstein, D., Akhunov, B., Chin, A., Chol, D.W., Fenton, R.D., Kianian, P., Otto, C., Simons, K., Zhang, D., Bequm, D., Frisch, D., Yu, Y., Henry, D., Pelmer, M., Rambo, T., Simonns, J., Oates, R. and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cDNA library

Contact: Wing RA

Clease. The contact RA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCAGCTICACGGGCGCCTICGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCC 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1156 GGTACTCATCGGCTGGAGATGAAGAGGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGA 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976 ACCACGGCATCGAGGCGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCA 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1216 AGCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGTGTACTCGCGCTACTGCCACGAGA 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 CCAGCAGCTTCACCGGCCGGTTCGCGTCCCAAGCTGCCCTGGAAGAGAGACCCCTCTTTC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 CCGAGGTGACGCCCTCGTCGCGAGGCCTGCGACGCCTTCTTCCAGGTCGTCA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751 TGGTGGTGCAGCAGCAGCAGGAGGTGGTGTTCGACGCGCCGGTGCTGAGCGGGCAGACGG 810
                                                                                                                                                                                         811 AGAICCCGTCGCAGTICATATGGCCGGCGGAGAGACCCCCGGGTCGGTGGCGGTGGAGG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AGATGCACGTCCCGCTCATCGACATCGGCGGCATGCTCCCGCCGACCCCCGCGGGCCG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      918 TC--GGTGGTCCGCCAGGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTA 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- GGCGGGGGGGAGAGGTCG 917
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                      30;
Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1276 TGAGCCGCCTGTCGCTGGAGCTGAT-GGAGGTGCTCGGGGAGAGCCTGGG 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACCCGGCTGTCCCTGGAAAACATGGGAGGGGCTCGGGAAGAACCCTGG 704
                                                                          Indels
DB 12;
                                                                          0; Mismatches 156;
Score 230.4; DB 1
Pred. No. 5.7e-37;
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                     871 AGCIGGAGGIGGCGCIGAICGACGIGGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG416635
BG416635.1 GI:13322186
9.2%;
                                                                  Matches 404; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare.
                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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Query Match
                                       Local
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AUTHORS
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SOURCE
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BG416635
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Gaps

3;

120;

Length 682; Indels Ĥ

Gaps

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BE454826 571 bp mRNA linear BST 22-OCT-2001 HVSMBD0095D08f HOrdeum vulgare 5-45 DAP spike BST library HVCDNANO099 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMBh0095D08f, BE454826
                                                                                                                                                                                                                                          1411 AGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCATCC 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1531 GCCCTCGCCCCGGGGCGCTCGTCGTCAACGTCGGCGACACCTTCATGGCGCCTCTCCAACG 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1651 TGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCGCCCCCCCGGAGGAGCTGGTCG 1710
                                                                                                                                                                                                                                                                                                                                                            1591 CCAGGTACCGCAGCTGCCTGCACCGGGGGGTGGTCAACAGCACGGCGCCTCGCCGCGCTCGC 1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1711 AC---GACCACCACCGAGGGTGTACCCGGACTTCACGTGGCGGGGGCGTGCTGGACTTCA 1767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1768 CGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAATC 1827
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
186 c 161 g 98 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                              122 GGCCCGGAGCGACGCCTTCGTCGTCAACATCGGCGACACTTCTCGGCGCTCACCG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 GGCGCCACGTCCACCGCCCCCCACGCGCGCGCGCGCCCGCAGGTCGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 CGCAGAAAGCACTACCGCTCTGACTCCTGGATGCCTTCGCGCTTGGATCAATC 421
                                                                                                                                                                                                                                                                                                 2 AGAAGCCTCACCTGACGCTGGGCACGGGCCCGCACGACGGCGCGCTGACGCTGC 61
                                                                                                                                                                               3;
                                                                                                                        Length 566;
                                                                                                                 Score 209.8; DB 12; Length
Pred. No. 1e-32;
0; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
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Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: AATIAACCELLE
High quality sequence stop: 556.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE454826.3 GI:16322121
                                                                                                                     1 8.4%;
Similarity 70.3%;
                                                                                                                                                                            Matches 296; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare.
                                 120 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1828 A 1828
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                                                                                                                        Query Match
                                                                                                                                                   Best Local
                              BASE COUNT
ORIGIN
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BE454826
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AUTHORS
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KEYWORDS
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/Clone_lib="Howaracoullill"
/Clone_lib="Howaracoullill"
/Lab_bost="Total"
/Lab_
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 566)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., Von Wing, R., Close, T.J., Kleinhofs, A., Choi, D.M., Fenton, R.D., Kianian, P., Otto, C., Simons, K., Zhang, D., Bequm, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simons, J., Oates, R., and Main, D. Development of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cDNA library
                                                                                                                                                                                                                                       BG414208 566 bp mRNA linear EST 23-OCT-2001
HVSMEk0001C12f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0001C12f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total hq bases = 168
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence start: 9
High quality sequence stop: 545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Morex" /db_xref="taxon:4513" /clone="HVSMEk0001C12f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                            BG414208
BG414208.1 GI:13319759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare.
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                              1828 A 1828
                                                                                         422 A 422
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DEFINITION
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                                                                                                                                                                            RESULT 9
BG414208
                                                                                                                                                                                                                                                                                                                                                            ACCESSION
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KEYWORDS
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FEATURES

TITLE

SOURCE

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae
                                                                                      EST 25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943 CGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGCGCTGCTGCTGG 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003 AGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGGAGAAGCAGCGGG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1063 CGCAGCGGCGCGGGGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGCGT 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1123 CCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGGAGATGAAGAGG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 TCGCCGGGTTCCTGGCGGGCGCGCCGCCACCTGGCGGCCCTCCGTGACCTGGCCGCCG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406 GCAAGCTCCCCTGGAAGGAGCAGCCTCTCTAACTGCTCCGCCGCCGCCGAGGGCGCCC 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 CAGCCGACGAGGCCCCGTCCGTCGACGGCGTGGAGAGATCGCCGTCCCGGTCGACA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 CGCAGCGCCCCCCCGCGAGAACCACGGGTACGCCGGCAGCTTCGTGGGGCGGTTCGGCA 405
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                                                               567 bp mRNA linear EST 25-JUN BRI_2428 wheat EST endosperm library Triticum aestivum cDNA 5' BQE06563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carnegie Institution of Washington, Dept. o 260 Panama Street, Stanford, CA 94305, USA 121 1 650 325 1521 x 251 Fax: 1 650 325 3748 Email: rhee@acoma.stanford.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 200; DB 14;
Pred. No. 1e-30;
0; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                  Clarke, B., Lambrecht, M. and Rhee, S. Assessing the utility of Arabidopsis interpreting wheat EST sequences Unpublished (2002)
Contact: Lambrecht M
The Arabidopsis Information Resource
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/db_xref="taxon:4565"
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                                                                                                                                                                               BQ606563.1 GI:21555890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 202 c 190 g 87 t
                                                                                                                              /clone_lib~"Hordeum vulgare 5-45 DAP spike EST library
VPDDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1132 CGTGGAAGGACGCTGTCCTTCCGGTACTCAFCGCCTGCAGATGAAGAGGCGCAGGAGG 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTGCTGGTGGAGGAGGCGC 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072 GCGCGGGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGCGTCCAAGCTGC 1131
                                                                                                                                                                                                                      /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
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Pred. No. 1.7e-31;
0; Mismatches 127; Indels
                                            'organism="Hordeum vulgare"
                                                                                                             /clone="HVSMEh0095D08f"
                                                               /cultivar="Morex"
/db_xref="taxon:4513"
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Best Local Similarity 69.3%;
Matches 293; Conservative
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1720 ACCCGAGGGTGTACCCGGACTTCACGTGCCGGGCGCTGCTGGACTTCACGCAGCGCCCACT 1779
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                           BG350197 655 bp mRNA linear EST 01-N
084C04 Mature tuber lambda ZAP Solanum tuberosum CDNA, mRNA
Emmersen, J. and Welinder, K.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                              1243 TGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGG 1293
                                                                                                                                                                                                                                                                                                                              1 (Dases 1 to 655)
Nielsen,K.L. Crookshanks,M., Emmersen,J. and Wellin
EST-sequencing of mature potato tuber (Var. Kuras)
Unpublished (2000)
Contact: Karen G. Welinder
Institut for bioteknologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 others
                                                                 Pred. No. 4.5e-30;
0; Mismatches 174; Indels
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Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Solanum tuberosum'/cultivar="Field grown Kuras"
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/note="Vector: Lambd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +45 96358467
Fax: +45 98141808
Emall: Kgw@blo.auc.dk
Sequenced from the 5' end.
High quality sequence stop:
                                                                                                                                                                                                                       GI:13178939
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Best Local Similarity 63.3%;
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Trittoum aestivum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaleae;
Triticaea; Triticum.
1 (bases 1 to 517)
Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia
C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
                                                                                                                                                                                                                                                                                       BE422495 517 bp mRNA linear EST 24-JUL-2000 WHE0056_E02_104ZS Wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0056_E02_104, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Lambda ZAP II, excised phagemid; Site_1: BcoRI; Seeds collected, endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1460 GCTCACCATCCTCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGCGGAGGGGGCGGTG 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1520 GCGCGCCATCCGCCCTCGCCCCGGGGCGCTCGTCAACGTCGGCGGACACCTTCATGGC 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1580 GCTCTCCAACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACACACGCGGCGCC 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence have been trimmed to remove vector sequence and low quality sequence with pired score less than 20 Seq priner: Stratagene SK primer. Location/Qualifiers
1780 ACAGGGCCGACATGCGCACGCTTCAGGCCTTCCCGACTGGCTTAATCATCATC 1833
                                                                                                                3,
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Pred. No. 6.6e-29;
0; Mismatches 103; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Cheyenne"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0056_E02_104"
/clone=lib="Wheat endosperm cDNA library"
/tissue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E, coli SOLR"

    .517
    /organism="Triticum aestivum"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                              BE422495
BE422495.1 GI:9420410
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Best Local Similarity 71.5%;
Matches 266; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bread wheat.
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Duraryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosidas II; Malvales; Malvaceae; Gossypium.

1 (Dases 1 to 700)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leelie,A. and Wilkins,T.A.

In the ootton fiber
Unpublished (2000)
Contact: Wing R.

Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ402912 700 bp mRNA linear EST 22-MAY-2005 GA__Bd0052C12f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA__Ed0052C12f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar="8400"
/db_xref="taxon:99729"
/clone="64_R0052cl2f"
/clone=1ch="cossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                               CGCAGCGGGGGGGGGGGAGAGCTGCGGCTACGCCAGCTTCACGGGGCGCTTCGCGT 1122
                                                                                  943 CGIGCGAGAGGCACGGCTICTICCTGGTGGTTAACCACGGCAICGAGGCGGCGCTGCTGG 1002
                                                                                                                                                                       1003 AGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAAGCAGCGGG 1062
                                                                                                                                                                                                                                                                                                                                                  1123 CCAAGCTGCCGTGGAAGGAGACGCTGTTCGTTCCGGTACTCATCGGCTGGAGATGAAGAGG 1182
                         279 TCGCCGGGTTCCTGGCGGGCGACGGCGCTGCCACTGGCGGCCTCCGTGACCTGGCCGCCG 338
                                                                                                                                                                                              459 CGCAGCGCCCTCGGCGAGAACCACGGGTACGCCGCAGCTTCGTGGGGCGGGGTCGGCA 518
                                                                                                                                                                                                                                                                                                                                                                           TGG------GGGCGGGGGGGGGGGGGTCGTCGGTGG--TCCGGCAGGTGGGGGAGG 942
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Pred. No. 8.8e-28;
0; Mismatches 230; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI" 148 c 171 g 186 t 1 others
                                                                                                       100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Total High Quality bases = 572
Seq primer: TRATRGGACTCACTATAGGG
High quality sequence start: 7
High quality sequence stop: 680.
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1. .700
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BQ402912.1 GI:21090599
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Best Local Similarity 59.9
Matches 371; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         1183 GCGAGGAGGGCG 1194
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AUTHORS
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BQ402912
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 24-JUL-2000
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Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Holton T'
Centre for Plant Conservation Genetics, Southern Cross University
PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
           1757 GCTGGACTTCACGCAGCGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGA 1816
                                  217 CCTCGAGTTCACGCAGAAGCACTACCGCTCTGACTGGAGGACCCTGGATGCATTCGCCTC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 IGGIGITICGACGCGGCGGTGCTGAGCGGGCAGACGGAGATCCCGTCGCAGTTCATATGGC 834
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SCU007.E01.R990714 ITEC SCU Wheat Endosperm Library Triticum
aestivum cDNA clone SCU007.E01, mRNA sequence.
                                                                                                                              277 CGAGCTGCTCGCCGCGCGCGCGCGCGTGTACCCCGGGCTTCACTTGGCGTGAATT
                                                                                                     Pred. No. 4.6e-28;
0; Mismatches 126; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /do_are=__cuo07.E01"
/clone_lib="ITEC SCU Wheat Endosperm Library"
/tissue_type="endosperm"
/note="Vector: Bluescript II SK(-)"
a 232 c 232 g 105 t 5 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tholton@scu.edu.au
International Triticace EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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Pred. No. 4.6e-28;
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/db_xref="taxon:4565"
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Best Local Similarity 68.1%;
Matches 294; Conservative
                                                                                                                                                                                                                                                                               1817 CTGGCTTAATCA 1828
                                                                                                                                                                                                                                                                                                               157 GTGGATCAATCA 146
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BE414214
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KEYWORDS
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EST 22-MAY-2002

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1168 CTGGAGATGAAGAGGCGGAGGAGGGCGTGGGTGACTACCTGGTGCGGAAGCTCGGGGCGG 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1348 ACTICCGGCGATICTTCCAGCGCAACGACTCCATCATGCGCCTCAACTACTACTACCGGCGT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1408 GCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCACCTCGCTCACCA 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1468 TCCTCCACCAGGACCACGTCGGCGCCTGGAGGTGTGGGGCGGAGGGGCGGTGGCGGCGTA 1527
                                                                    988 AGGCGCCCCCCCCGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGG 1047
                                                                                                                                      1048 GGGAGAAGCAGCGGCGCGCGCGCGCGGGGGAGAGCTGCGCCTACGCCAGCAGCTTCA 1107
                                                                                                                                                                                                         1108 CGGGGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGACGCTGTCGTTCCGGTACTCATCGG 1167
                                                                                                                                                                                                                                                                                              220 AFGATAAGCAAAGGCTCAGAGGAAACTTGGTGAGCACTGTGGGATATGCTAGTAGCTTCA 279
                                                                                                                                                                                                                             394 AATTC---AAGCATTTCGGCAGGGTTTACCAAGATTACTGCGAGCCAATGAGCAAGCTAT 450
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Search completed: March 26, 2003, 07:52:50 Job time : 2570.09 secs

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March 26, 2003, 04:38:30 ; Search time 61.8613 Seconds
(without alignments)
12398.686 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUG_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUG_COMB.seq:*
GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-359-081-2
US-09-359-081-2
US-09-130-114-1
US-08-910-647-1
US-09-620-925-1
US-07-884-811-15
US-07-885-971-15
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Maximum DB seq length: 2000000000
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Perfect score:
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Patent No. 259559
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: 6A 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
US-08-458-298-1
US-09-454-034-9
US-09-53-3674-12
US-09-734-719-12
US-09-75-907A-1
US-08-765-907A-1
US-08-765-907A-1
US-08-765-907A-1
US-08-217-844B-1
US-08-217-844B-1
US-08-218-14
US-08-218-14
US-08-784-385-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-1
US-08-823-986A-3
US-08-823-986A-3
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US-09-615-192A-149
US-09-010-928B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 593539ember 27, 1995
CLASSIPICATION: 800
PRIOR APPLICATION DATA:
PRULICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REPERBENCE/DOCKEY NUMBER: 49/FD4.5MZ
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-721-8200
TELECHONE: 202-721-820
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| INMEDIATE SOURCE:
| CLONE: pat2301
| CLONE: Pat2301
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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COUNTRY: U.S.A.
ZIP: 20006
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STATE: D.
COUNTRY:
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Lind & Ponack, L.L.P. N.W., Suite 800
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COMPUTER READABLE FORM:
COMPUTER: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS_DOS
                                                                                                                                                                                                                                                                                                        27,
                                                                                                                                                                                SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/295,306
                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6198021ember 7
ATTORNEY/AGENT INFORMATION:
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nilarity 60.0%;
Conservative 0
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SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                   2033 K Street,
                      Wenderoth,
 CORRESPONDENCE ADDRESS:
                                 STREET: 2033 K St
CITY: Washington
                                                                    D.C.
: U.S.A.
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ORIGINAL SOURCE:
ORGANISM: Arab
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Matches 532;
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                                                                                                                                                                                                    CGGGCGCAGCGCGCGCGCGCGAGAGCTGCGGCTACGCCAGCAGCTTCACGGGCCCCTTC 1118
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                                                                                                                                    CTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGAGAAGCAG 1058
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                                                                 939 GAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTG 998
                                                                                      324 AIAICAGACGCTCATGAATACACGAGCCGCTTCTTTGATATGCCTCTCTCCGAAAAACAG 383
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APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
   Length 1259;
                                   Indels
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Score 292.4; DB 2;
Pred. No. 2.2e-54;
0; Mismatches 336;
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Patent No. 6198021
 11.7%;
60.0%;
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US-09-295-306-3
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Pred. No. 2.2e-54;
0; Mismatches 336;
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                                                                                      GATCTCACACAGAACAGGACCTCATTGTGATCCAACATCTCTTACCATCCTTCACCAA 785
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1359 TICITCCAGCGCAACGACTCCATCATGCGCCTCAACTACTACCGGCGTGCCAGAGGCCA
                      1419 CTCGACACGCTGGGCACCGGTCCGCACTGCGACCCCCACCTCGCTCACCATCCTCCACCAG
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APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19-
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ADDRESSER: Wenderoth, Lind & Ponack, L.L.P.
STREF: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: April 21, 1999
APPLICATION NUMBER: 08,553,367
FILING DATE: No. 6455675ember 27,
APPLICATION NUMBER: PCT/EP94/01664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/734,719
FILING DATE: 13-Dec-2000
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APPLICATION NUMBER: 09/295,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09734719
Patent No. 6455675
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NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-721-8250
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US-09-734-719-3
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Pred. No. 2.2e-54;
0; Mismatches 336;
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                                                                                                                                                                                                                                                                 ORIGINAL SOURCE: ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                           CLONE: PAt2301
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                 LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                  SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 3:
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60.0%;
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Matches 532; Conservative
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958 GCTICTTCCTGGTGGTTAACCACGGCATCGAGGCGGCGCTGCTGGAGGAGGCGCACCGGT 1017
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Patent No. 6198021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDAS
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CORRESPONDENCE ADDRESS:
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US-09-295-306-5
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                                                                                                                                                     Sequence 5, Application US/08553367A
Patent No. 283953
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TILLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 271; DB 2; Length 1490;
Pred. No. 1e-49;
0; Mismatches 435; Indels 2
                                                               1086 TATAGAGCAGACATGAACACTCCCAAGCCTTTTCAGATTGGCTCA 1131
                                             1779 TACAGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTA
                                                                                                                                                                                                                                                               Wenderoth, Lind & Ponack, L.L.P. 33 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                    E: Diskette, 3.5 inch, 1.44 mb
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CUBRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/553,367A
FILING DATE: NO. 5939539emDer 27, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 40,949
REFERENCE/COCKET UNHBER: 49/FD4.5MZ
TELECOMMUNICATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                         STREET: 2033 K Street, N.W., CITY: Washington STATE: D.C.
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Best Local Similarity 56.5
Matches 593; Conservative
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STRANDEDNESS: sing
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MOLECULE TYPE:
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US-08-553-367A-5
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586 AAGAITACTITTCCGATACATTAGGACAAGAGTTCG---AGCAGTTTGGGAAGGTGTATC 642
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FILING DATE: 13-Dec-2000
CLASSIFICATION: <UNKnown>
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SOFTWARE: Wordperfect 5.1
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Patent No. 6455675
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                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 40,949
REFERRNCE/DOCKET NUMBER: 49/DIV-FD4.5MZ
TELECOMMUNICATION INFORMATION:
TELEFRONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6198021ember 27, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 COMPUTER: IBM Compatible
                                                                                                                                      SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
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56.5%;
                                                                                                      COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: MS-DOS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1490 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                    COMPUTER READABLE FORM
              D.C.
: U.S.A.
Washington
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                                                                                                                                                                                                                                                                                                    NAME: Lee Cheng
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ORIGINAL SOURCE:
                                                                                                                                                                                            FILING DATE:
                                                20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-09-295-306-5
                                   COUNTRY:
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1258 CGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGGAGCTGATGGAGGTGCTCGGGGGAGA 1317
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                                                                                                                            GCCIGGGCAICGICGGAGACCGGCGCCCACIACTICCGGCGAIICITCCAGCGCAACGACI 1377
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                                                      643 AAGACTATTGTGAAGCAATGAGTTCTCTATCACTCAAGATCATGGAGCTTCTGGGCTTAA
                                                                                                                                                                                         703 GITTAGGCGTAAACCGAG-----ACTATTTCCGAGGATTTTCGAAGAGAACGATT
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APPLICANT: Theodox LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (AS Amended)
NUMBER OF SEQUENCES: 19
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COMPUTER READABLE FORM:
MEDIUM IYPE: Diskette, 3.5 inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/295,306
FILING DATE: APT11 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: NO. 6455675ember: 27,
APPLICATION NUMBER: PCT/EP94/01664
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1438 GICCGCACIGCGACCCCACCICGCICACCAICCICCACCAGGACCACGICGGCGGCCIGG 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-721-8250
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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CLASSIFICATION: 800
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US-08-553-367A-1
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                                                 REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/JC/01784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEFAX: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 271; DB 4
Pred. No. 1e-49;
                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                               CLONE: PAT2353
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
FILING DATE: May 24, 1994
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRRACTERISTICS:
LENGTH: 1490 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                 ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.8%;
Best Local Similarity 56.5%;
Matches 593; Conservative
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CGGTTGTGAATAGAGAGAGGCGCGAGAAATCGATGGCGTTTTTTCTTGTGTCCGAAGAAG 1053
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                                                                            AGGIGIGGCGGAGGGCGGTGGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCA 1557
                                                                                                                                                                                     CGGTCGTCAACAGCACGCCCTCGCCTCGCTGGCCTTCTTCTTCTTCTTCTGCCCGGAGATGG 1677
                                                                                                                                                                                                                                                                                                                                                                                                                 ACACGGTGGTGCCCCCCCCCGCAGGAGCTGGTCGACCACCACCCGAGGGTGTACCCGG 1737
                                                                                                               934 ATATIGGIGACACTITCATGGCICTATCGAACGGGATATTCAAGAGCTGTTTGCATAGAG 993
Sequence 1, Application US/08553367A
Patent No. 5939539
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
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COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
FILING DATE: NO. 5939539ember 27, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTTCAGGCCTTCTCCGACTGGCTTAAT 1826
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NAME: Lee Chenq
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TYPE: nucleic acid
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                                                                                                                         Length 1395;
                                                                                                                                                                Indels
                                                                                                                           DB 2;
                                                                                                                       Score 226.4; DB 2
Pred. No. 4.5e-40;
0; Mismatches 381
                   ORGANISM: Cucurbita maxima IMMEDIATE SOURCE: CLONE: Clone pB11
                                                                                                                       9.1%;
nilarity 55.2%;
Conservative 0
                                                                                                                     Query Match
Best Local Similarity
Matches 496; Conserv
ORIGINAL SOURCE:
ORGANISM: CUC
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US-08-553-367A-1
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RESULT 8 US-09-295-306-1

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Sequence 1, Application US/09295306
Patent No. 6198021
GENERAL INFORMATION:
APPLICANT: Theodor LANGE et al.
TITLE OF INVENTOR: GA 20-OXIDASE GENE SEQUENCES (As Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1395;
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55.2%; Pred. No. 4.5e-40;
tive 0; Mismatches 381;
                                                                                                                                                     Lind & Ponack, L.L.P., N.W., Suite 800
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REGISTRATION NUMBER: 40,949
REGISTRATION NUMBER: 49/DIV-FD4.5MZ
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APPLICATION NONBER: 08/553,367
FILING DATE: NO. 6198021ember 27, 1995
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                         inch, 1.44
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/295,306
                                                                                                                                                                            2033 K Street, N.W.,
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nucleic acid
DEDNESS: single
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
                                                                                                                                      CORRESPONDENCE ADDRESS
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CLONE: Clone pB11
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Best Local Similarity
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RY: U.S.A.
20006
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                    STATE: D. COUNTRY:
                                                                                                                                                                                                                                                                                                                             COMPUTER;
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1588 ACGCCAGGTACCGCAGCTGCCTGCACCGGGCGGTCGTCAACAGCACGGCGCCTCGCCGCT 1647
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TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (AS Amended)
NUMBER OF SEQUENCES: 19
                                                                                                                    595 GTACGAAGATTGTGGAGCTTTTGGGGCCTTTGGCCATTTCAAGAG-----AAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/295,306
FILING DATE: April 21, 1999
APPLICATION NUMBER: 08/553,367
FILING DATE: No. 6455675ember 27, 1995
APPLICATION NUMBER: PCT/EP94/01664
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SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09734719
Patent No. 6455675
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
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ZIP: 20006
COMPUTER READABLE FORM:
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988 AGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGG 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646 ACTICAAGAATITICITICGAGGACAACGATICAATATIGAGGCITAATIACTACCAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 2000-1678/IC/01784
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 226.4; DB 4
Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        CLONE: Clone pB11
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                ORGANISM: Cucurbita maxima
                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1395 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.18;
                                                                                                             TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 496;
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                                                                                         1006 TGGAGAAGAGTCCACCACGAAAGTATCCAGATTATAAATGGCCAATGTTGCAGTTGAAATGA 1065
                     1172 AGAIGAAGAGGCCGAGGAGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGAGCA 1231
                                                                 TCGACGACCACCACCGGAGGGTGTACCCGGACTTCACGTGGCGGGGGCGCTGCTGGACTTCA 1767
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1648 CGCTGGCCTTCTTCCTCTGCCCGGAGATGGACACGGTGGTGCTGCCCCGCCGGAGGAGCTGG 1707
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                                                                                                                                   GGCAGGGCCACTACAGGGCCGACATGCGCACGCTTCAGGCCTTCTCCGACTGGCTTAA 1825
                                                                                                                                                                    1066 CCCAAAAGCGTTACCGACCTGATTGCAACACTTTGGAAGCCTTCAAAACTTGGGTTCA 1123
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOTLICK, Robert
TILLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
FILE REFERENCE: 0867/0905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SOFFWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1926;
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49.2%; Pred. No. 1.9e-11;
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CHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
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Patent No. 6417002
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US-09-249-585A-2
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992 GGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGGA 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2580;
                                                     GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 94.4; DB 3; Length 2
Pred. No. 2e-11;
0; Mismatches 256; Indels
                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDION TYPE: Ploppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS
TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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LENGTH: 2580 base pairs
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Matches 248; Conservative
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E: DNA
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US-09-050-863-2
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US-09-050-863-2
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Best Local Similarity 49.2
Matches 248; Conservative
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ORGANISM: VEBNA
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                                                           GAICCCGICGCAGIICAIAIGGCCGGCGGAGGAGCCCCCGGGICGGIGGCGGIGGAGGA 871
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                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mammalian Protein Interaction Cloning System
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ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPURER READABLE FORM:
COMPUTER: USA
COMPUTER: FLORM:
COMPUTER: FLORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,081
FILING DATE: 22-01-1999
CLASSIFTCATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/050,863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 94.4; DB 4;
Pred. No. 2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-359-081-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                   1173 GGAGGGCAGGAGGGCAGGAGCA 1196
                                                                                                                                                       1232 CGGCGGCGCTGGGCGAGGTGTA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 2580 base pairs
                                                                                                                                                                                                                                                             Sequence 2, Application US/09359081
Patent No. 6316223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.8%;
                                                                                                                                                                                                                                                                                                    APPLICANT: Lao, Ying
Hiang, Betty
Payan, Don
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                            INFORMATION:
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Best Local Similarity
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US-09-359-081-2
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                                                                                                                                                                                                                                                                                                                                                                                                               AGATGAAGAGGCGAGGAGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGAGCA 1231
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                                                                                                                                                                                                             GCTGGAGGTGGCGCTGATCGACGTGGGGGGGGGGGGGGAGAGGTCGTCGGTGGTCCGGCA
                                                                                                                                       GGTGGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC
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Batent No. 5976807

GENERAL INFORMATION:
APPLICANT: BOTICK, Robert A.
APPLICANT: Danaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Erom Multiple Transfected Episomes
TITLE OF INVENTION: Erom Multiple Transfected Episomes
CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06
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Pred. No. 2.6e-11;
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SOFTWARE: FastSEQ for Windows Version 3.0
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1112 GCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGCTGTCGTTCCGGTACTCGGCTGG 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                        992 GGCGCTGCTGCAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGA 1051
                                                                                                                                                                                                                                                                                                                                                                                                 1172 AGATGAAGAGGCGAGGAGGGCGTGGGTGAGTACCTGGTGCGGAAGCTCGGGGCGGAGCA 1231
    932 GGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zuckermann et al. TITLE OF INVENTION: Compositions and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynuclectide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <URNOWn>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1218.002
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/910,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4560 Horton Street CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1219 GGAGGGCAGGAGGGCAGGAGCA 1242
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TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1232 CGGCCGCCGCTGGGCGAGGTGTA 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-620-925-1
; Sequence 1. Application US/09620925
; Patent No. 668986
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 9600 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California COUNTRY: U.S.A. ZIP: 94608-2916 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                              1172 AGAIGAAGAGGCGAGGAGGCGIGGGIGAGIACCIGGTGCGGAAGCICGGGGCGGAGCA 1231
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                                      1052 GAAGCAGCGGGCGCAGCGCGCGCGCGGGAGAGCTGCGGCTACGCCAGCAGCTTCACGGG
                                                                                                                       1112 GCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGACGCTGTCGTTCCGGTACTCATCGGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions and Methods for Polynucleotide Delivery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.8%; Score 94.4; DB 4;
49.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 256;
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APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                       1232 CGGCGGCGGCTGGGCGAGGTGTA 1255
                                                                                                                                                                                                                                                                                                                              1632 GGAGGGCAGGAGGGCAGGAGCA 1609
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-910-647-1; Sequence 1, Application US/08910647; Patent No. 6251433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chiron Corporation
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IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fulita, Sharon M. REGISTRAITON NUMBER: 38,459 REFERENCE/DOCKET NUMBER: 12. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zuckermann et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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Matches 248; Conservative
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ADDRESSEE: Chiron Co
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CITY: Emeryville
STATE: California
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                                                                                                                                                                                         932 GGTGGGGGAGGCGTGCGAGAGGCACGGCTTCTTCCTGGTGGTTAACCACGGCATCGAGGC 991
                                           812 GATCCCGTCGCAGTTCATATGGCCGGCGGAGAGAGCCCCGGGTCGGTGGCGGTGGAGGA 871
                        Gaps
                       0;
3.8%; Score 94.4; DB 4; Length 9600;
49.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 256; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 49.29
Matches 248; Conservative
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Search completed: March 26, 2003, 13:12:32 Job time : 97.8613 secs

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March 26, 2003, 05:23:30 ; Search time 137.899 Seconds (without alignments) 15433.627 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_DUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_DUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_DUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_DUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_LUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_LUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                                     OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 77, Appl	-	Sequence 71, Appl	Sequence 47, Appl	Sequence 8, Appli	Sequence 1829, Ab	Sequence 812, App	Sequence 1511, Ap	Sequence 5184, Ap	Sequence 2672, Ap	Sequence 20699, A	Sequence 19241, A	Seguence 2513, Ap	Sequence 5, Appli	Sequence 4, Appli	Sequence 20241, A	Sequence 3471, Ap	Sequence 1691, Ap	Sequence 645, App
3 ID	LO US-09-371-307-77	10 US-09-371-307-8	10 US-09-371-307-71	9 US-10-032-393-47	9 US-10-032-393-8	10 US-09-923-876-1829	9 US-09-938-842A-812	9 US-09-938-842A-1511	10 US-09-294-093B-5184	9 US-09-938-842A-2672	10 US-09-864-761-20699	10 US-09-864-761-19241	10 US-09-864-761-2513	10 US-09-371-307-5	10 US-09-969-852-4	10 US-09-864-761-20241	10 US-09-864-761-3471	9 US-09-938-842A-1691	10 US-09-887-576-645
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% Query Match	9.1	6.1	5.2	3.4	3.4	3.2	3.2	3.0	2.9	2.9	2.9	2.9	2.9	2.9	2.9	2.7	2.7	2.7	2.7
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APPLICANT: Brown, Sherri M.
APPLICANT: Piller, Kenneth J.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Ligh, Tedd D.
APPLICANT: Logusch, Eugene W.
APPLICANT: Rean, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Logusch, Sherry J.
TITLE OF INVENTION: Methods for controlling gibberellin levels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1394 CTACTACCGGCGTGCCAGAGGCCACTCGACACGCT---GGGCACCGGTCCGCACTGCGA 1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1688 GCGCCCGCCGGAGGAGCTGGTCGACGACCACCCCGAGGGTGTACCCGGACTTCACGTG 1747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 CACCCTGCAGGTGTTGACGAACGGGAGGTTCAGGAGCGTGAGGCACAGGGTGGTGGTGGTGAA 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                  APPLICANT: Logucch, Bugene W.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
APPLICANT: Ream, Joel E.
TITLE OF INVENTION: Methods for controlling gibberellin levels
FILE REFRENCE: MOBF:216
CURRENT APPLICATION NUMBER: US/09/371,307A
CURRENT PILING DATE: 1999-08-10
NUMBER OF SEQ ID NOS: 89
SOSTWARE: Patentin Ver. 2.0
SEQ ID NO 71
                                                                                                                                                                                                                                                                                                                                                                                                              Length 811;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Score 129; DB 10;
Pred. No. 1.9e-24;
0; Mismatches 205;
Sequence 71, Application US/09371307A
Patent No. US20020053095A1
GENERAL INFORMATION:
APPLICANT: Brown, Sherri M.
APPLICANT: Heck, Gregory R.
APPLICANT: Piller, Kenneth J.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Elich, Tedd D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-10-032-393-47
'Sequence 47', Application US/10032393
; Publication No. US20030027286A1
                                                                                                                                                                                                                                                                                                                                                                                                            5.2%;
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Matches 278; Conservative
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ORGANISM: Zea mays
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1071 CGCGCGGGGGAGAGCTGCGGCTACGCCAGCTTCACGGGGGGGCGTTCGCGTCCAAGCTG 1130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   771 GAGGTGGTGTTCGACGCGCGGTGCTGAGCGGCCAGACGGAGATCCCGTCGCAGTTCATA 830
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APPLICANT: Haselbeck, Robert
APPLICANT: Wall, Daniel
APPLICANT: Gross, Molly
TITLE OF INVERTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT PELLING DATE: 2010-112-21
PRIOR APPLICATION NUMBER: 60/259,434
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
SRIOR FILING DATE: 2000-09-06
SRIOR FILING DATE: 2000-09-06
SOFTWARE: FASEEQ for Windows Version 4.0
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Pred. No. 9.2e-12;
0; Mismatches 342; Indels
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; OTHER INFORMATION: Vector pEPEF14
US-10-032-393-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.45
Best Local Similarity 45.95
Matches 290; Conservative
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0;

Fri Mar 28 13:40:48 2003

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Score 81.2; DB 10; Length
Pred. No. 6.6e-12;
0; Mismatches 58; Indels
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CURRENT FILING DATE: 2001-08-24
PRICA APPLICATION NUMBER: US 60/227,866
PRICR FILING DATE: 2000-08-24
PRICR FILING DATE: 2001-01-16
PRICR FILING DATE: 2001-01-16
PRICR FILING DATE: 2001-01-05
PRICR FILING DATE: 2001-01-05
PRICR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 5379
Sequence 812, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                            Sequence 1829, Application US/09923876
Patent No. US20020013958A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.2%;
Best Local Similarity 67.9%;
Matches 129; Conservative
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US-09-938-842A-812
                                                                                                          -09-923-876-1829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%; Score 84.8; DB 9; Length 12739; Best Local Similarity 45.9%; Pred. No. 9.2e-12; Matches 290; Conservative 0; Mismatches 342; Indels 0;
                                                                                                 APPLICANT: Haselbeck, Robert
APPLICANT: Mall, Daniel
APPLICANT: Mall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Wally
TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
FILE REFERENCE: ELITRA.010A
CURRENT APPLICATION NUMBER: US/10/032,393
CURRENT APPLICATION NUMBER: 60/259,434
PRIOR PLILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-109-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
PRIOR PLILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                        Sequence 8, Application US/10032393
Publication No. US20030027286A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Vector peper US-10-032-393-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12739
                    US-10-032-393-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ranigaki, Laura Y. (Ito)
APPLICANT: Ranigaki, Laura Y. (Ito)
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILLE REFERENCE: P. 10012-1 CON
CURRENT FILLING DATE: 2001-08-06
FRIOR FILLING DATE: 1999-04-21
FRIOR FILLING DATE: 1999-04-21
FRIOR FILLING DATE: 1999-06-05
FRIOR FILLING DATE: 1999-06-05
SOFTWARE: PERL PROGram
SEQ ID NO 1829
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APPLICANT: Kreps, Joe1
APPLICANT: Kang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAININ
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 CATGGGGTCAACTICTACCGGCGTGGAGCCGGAGCTCACGAGCTCACGGACTCACGGGC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GCACACCGACCCCAACGCGCTCACCATCCTGCTCATGGACCCGGACGTCGCCGGCCTGCA 185
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| NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20020013958A1 700159601H2
US-09-923-876-1829
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Gaps

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Length 1179;

Score 74.8; DB 9; Length L' Pred. No. 9.4e-10; 0; Mismatches 172; Indels

3.0%;

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1450 ACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTCGGCGGCCCTGGAGGTGTGGGGCGG 1509
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                                                                                                                                                                                                                                                                                                                                         1390 TCAACTACTACCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCG 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      860 GIGACGAGGICACCGITGAICCAICCCTGGCICTITIGITGTCAACGIAGGGGATC 919
                                                                                                                                                                                                                                                                                                                                                                            1510 AGGGCCGTGCCCCCATCCCCCTCGCCCCCGGGCCCTCGTCGTCAACGTCGGCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          920 ATCTCGAGATATTTAGCAATGGGAGGTATAAAAGCCTGCTACATAGGGTATTGGTGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 AGCCATCGCCGAAACTCGTCGATAAACATAATCCATCACAGTATATGGAC 1089
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1511
LENGTH: 1179
                                                                                                                                                                 ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.94
Matches 178; Conservative
                                                                                                                                                                                       US-09-938-842A-1511
                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1000 TGGAGGAGGCGCACCGGTGCATGGACGCCTTCTT----CACGCTGCCGCTGGGGGAGA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1114 GCTTCGCGTCCAAGCTGCCGTGGAAGGAGCGCTGTCGTTCCGGTACTCGCTTCGGCTGGAG 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1234 GGCGGCGGCGGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCCGCCTGTCGCTGG 1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651 AGGCGGTGCTGCTTCCGGAGCTGGAGGAGGAGGTGGAGGTGGAGGTTATGCTGCTTCTTCTGG 710
                                                                                                                                                                                                                                                                                                        111 CrarGCCGrdaraCrGGTTraaGTGCTGGTCTTGGTGTTGGTATTGGTGGTGGTCCTGG 170
                                                                                                                                                                                                                                                                                                                                                                                                            171 AGGAGGATCTGGTTACGGAGGTGGAAGCGGTGAAGGCCGTGGAGCTGGTGGGCATGGCGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 regrescerresagerecracesageresageresaseseresageresageresarraces 350
                                                                                                                                                                                                                                                          700 CCATCGGTTAATTAATTGATTGATAGCTAGATTATCAACAATTAATGAGCATGGTGGTGC 759
                                                                                                                                                                                                                                                                                                                                                              760 AGCAGGAGCAGGAGGTGGTGTTCGACGCGGCGGTGCTGAGCGGGCAGACGGAGATCCCGT 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 IGGCGCTGAICGACGIGGGGGGGGGGGGGGGGGGTCGICGGTCGTCCGGCAGGIGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             940 AGCCGIGCGAGGCACGCCTTCTTCCTGGTGGTTAACCACGCCATCGAGGCGGCGCTGC
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                                                                                                                                                                                                               9
                                                                                                                                                       Score 80; DB 9; Length 768;
Pred. No. 2.8e-11;
0; Mismatches 330; Indels
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Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
                                                TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                         3.28;
                                                                                                                                                       Query Match 3.2%
Best Local Similarity 46.7%
Matches 294; Conservative
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                                                                                ; ORGANISM: Arau:
US-09-938-842A-812
SEQ ID NO 812
LENGTH: 768
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLIVECEOTIDES AND POLIPEPTIDES DERIVED FROM CORN TASSEL
TITLE OF INVENTION: POLIVECTIDES AND POLIPEPTIDES DERIVED FROM CORN TASSEL
CURRENT PLICATION NUMBER: US/09/294,093B
CURRENT APPLICATION NUMBER: 1999-04-16
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SOFTWARE: PERL PROGRAM
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1390 TCAACTACTACCCGGCGTGCCAGAGGCCACTCGACACGCTGGGCACCGGTCCGCACTGCG 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335Al 700355956Hl
NAME/KEY: unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.9%; Score 73.2; DB 10;
56.2%; Pred. No. 9.7e-10;
iive 0; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: 52, 67
; OTHER INFORMATION: a, t, c, g, or other
US-09-294-093B-5184
                                      Sequence 5184, Application US/09294093B Patent No. US20010051335Al GENERAL INFORMATION:
APPLICANT:
Lalgudi, Raghunath, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
RESULT 9
US-09-294-093B-5184
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N: EXPRESED IN HEART, SIGNAL = 10

N: EXPRESED IN FETAL LIVER, SIGNAL = 14

EXPRESED IN LUNG, SIGNAL = 13

N: EXPRESED IN HELLOO, SIGNAL = 13

N: EXPRESED IN HELA, SIGNAL = 13

N: EXPRESED IN PLACENTA, SIGNAL = 13

N: EXPRESED IN PLACENTA, SIGNAL = 13

N: EXPRESED IN BLACK, SIGNAL = 13

N: EXPRESED IN BLACK, SIGNAL = 13

N: EXPRESED IN BRAIN, SIGNAL = 13

N: EXPRESED IN BRAIN, SIGNAL = 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION UNDRER: PCT/USO1/00662
PRIOR PILLORION NUBBER: PCT/USO1/00661
PRIOR APPLICATION NUBBER: PCT/USO1/00661
PRIOR APPLICATION NUBBER: PCT/USO1/00661
PRIOR PILLING DATE: 2001-01-30
PRIOR FILLING DATE: 2000-09-21
PRIOR FILLING DATE: 2000-09-21
PRIOR PILLING DATE: 2000-09-21
PRIOR APPLICATION NUBBER: US 09/608,408
PRIOR APPLICATION NUBBER: US 09/774,203
PRIOR PILLING DATE: 2000-08-30
PRIOR FILLING DATE: 2000-01-39
PRIOR FILLING DATE: 2000-01-39
NUMBER OF EEQ ID NOS: 49177
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 2089
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50.7%; Pred. No. 1.5e-09;
tive 0; Mismatches 170;
                                                                                                                                                                                                          FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
                                                   APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP
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INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
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Matches
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Range, Joel
APPLICANT: Shu, Fong
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US 609938,842A
PRIOR APPLICATION NUMBER: US 60,227,866
PRIOR APPLICATION NUMBER: US 60,264,647
PRIOR PLING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1442 GCACTGGGACCCCACCTCGCTCACCATCCTCCACCAGGACCACGTGGGCGGCCTGGAGGT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1502 GTGGGCGGAGGGCGGTGGCGCCCATCCGCCCTCGCCCCGGGGCGCTCGTCGTCACGT 1561
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                         1450 ACCCCACCTCGCTCACCATCCTCCAGGACCACGTCGGCGCCTGGAGGTGTGGGCGG 1509
                                                                                                                                1510 AGGGGCGGTGGCGCCCATCCGCCCTCGCCCGGGGCGCTCGTCGTCAACGTCGGCGACA 1569
                                                                                                                                                                                                                                         660 ACATAAAGACCCAACCGTTATCACTGTCCTTCTTCAAGACCAAGTCTCTGGGTTTGCAAGT 719
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                                                                                                                                                                     156 ATGETCAATGETACGAGGCCAAGTACGTGCCCGACGACTCATCGTCGTATATCGGCGATC 215
                                                                                                                                                                                                                                                                                               216 AGATCGAGATTTTCAGCAACGGGCCATACAAGGCGGTGCTGCACCGTACGACGGTGAACA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 CATGGCGTTTAACTAATCCGCCGTGTCCAGAACCCGAGCTAACTTACGGACTTCCCGG 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             720 CITTAAGGATGATAAATGGGTCGCTGTTAGTCCCAATTCCCAACACTTTCATCGTCAATAT
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                                                                       96 ACATGAGCACGCTCACCGTCCTCGTGCCAACGAGGTGCAGGGCTCCAGGTCTTCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73.2; DB 9;
Pred. No. 2.3e-09;
0; Mismatches 168;
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US-09-864-761-20699
; Sequence 20699, Application US/09864761
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2672, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana US-09-938-842A-2672
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illarity 50.9%;
Conservative
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Best Local Similarity
Matches 174; Conserv
                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-09-938-842A-2672
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LENGTH: 1050
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991 CGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACGCTGCCGCTGGGGGG 1050
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                                                                                                                                                                                                                                 CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 27

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19

OTHER INFORMATION: EXPRESSED IN ET474, SIGNAL = 34

OTHER INFORMATION: EXPRESSED IN FETAL LLVER, SIGNAL = 7.1

OTHER INFORMATION: EXPRESSED IN ADULT LLVER, SIGNAL = 7.3

OTHER INFORMATION: EXPRESSED IN ADLLA LLVER, SIGNAL = 28

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 20

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 25

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 18

OTHER INFORMATION: TALLASSOLL SIGNAL = 18
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                                                               SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 19241
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US-09-864-761-2513
US-09-864-761-2513, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
         PRIOR FILING DATE: 2001-01-29 NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                            TYPE: DNA
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Green, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                     978 CACGGCAICGAGGCGGCGCTGCTGGAGGAGGCGCACCGGTGCATGGACGCCTTCTTCACG 1037
                                                                                                                                                                                                                                          857
                                                                                                                                             73 GTGGCGGTGATGGTGGCGGTGGCAGTGGCGGTGGTGGTGGTGGTGGTGATG 132
918 ICGGTGGTCCGGCAGGTGGGGGGGGGGGGGGGCACGGCTTCTTCCTGGTGGTTAAC
                                                                                       798 AGCGGCAGACGGAGATCCCGTCGCAGTTCATATGGCCGGCGGAGGAGGCCCCGGGGTCG
                                                                                                                                                                                                      1038 CIGCCGCIGGGGGAGAAGCAGCGGGGGCGCGCGCGCGGGGGAG 1082
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PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR FILING DATE: 2000-05-24
PRIOR PRILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-30
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FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
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US-09-864-761-19241
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1111 GGCGCTTCGCGTCCAAGCTGCCGTGGAAGGAGGCGCTGTCGTTCCGGTACTCATCGGCTG 1170
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                                  931 AGGIGGGGAGGCGIGCGAGAGGCACGCCTICTICCIGGTGCTIAACCACGGCAICGAGG 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 7.1e-09;
0; Mismatches 186;
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CURRENT PPLICARION NUMBER: US/09/371,307A
CURRENT FILING DATE: 1999-08-10
NUMBER OF SEQ. ID NOS: 89
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SEQ ID NO 5
LENGTH: 1030
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                                                                                         TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: AGENICA-X-1
FILE REFERENCE: AGENICA-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT PILING DATE: 2001-05-23
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45.2%; Pred. No. 7.7e-09;
tive 0; Mismatches 319; Indels 0;
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N: EXPRESSED IN BONE MARROW, SIGNAL = 27
N: EXPRESSED IN LUNG, SIGNAL = 19
N: EXPRESSED IN BT474, SIGNAL = 34
N: EXPRESSED IN BT474, SIGNAL = 34
N: EXPRESSED IN BT474, SIGNAL = 7.1
N: EXPRESSED IN HELA, SIGNAL = 43
N: EXPRESSED IN HELA, SIGNAL = 20
N: EXPRESSED IN HELA, SIGNAL = 25
N: EXPRESSED IN HELA, SIGNAL = 25
N: EXPRESSED IN HEARY, SIGNAL = 18
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 2513
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-06-36
PRIOR FILING DATE: 2000-08-03
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00663
PRIOR PLICATION NUMBER: PCT/US01/00661
PRIOR PLILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                       Rank, David R.
Hanzel, David K.
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                                                                          Chen, Wensheng
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ATTLE OF INVENTION: A METHOD FOR ESTABLISHING AN EXPRESSION SYSTEM OF SPIDER DRAGLINE
TITLE OF INVENTION: A GENE IN BOMBYX MORI
TITLE OF INVENTION: A 2001-10-04
CURRENT APPLICATION NUMBER: CA01-10-04
PRIOR FILING DATE: 2001-10-03
NUMBER: OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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Patent No. US20020137211A1
GENERAL IMPORMATION:
APPLICANT: Liu, Tianyan
APPLICANT: Liu, Huifen
APPLICANT: Liu, Huifen
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Description

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AC096690 145999 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBA0059G06, *** SEQUENCING IN PROGRESS ***, 5 ordered pieces
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Oryza sativa.
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Oryza sativa.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bhrhartoideae; Oryzaeae; Oryza.

1 (bases 1 to 145999)

Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                   SUMMARIES
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AUTHORS
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(without alignments)
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       GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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5001
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                                                                                                                                                                                                        2054640 seqs, 14551402878 residues
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Listing first 45 summaries
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AC096690 Oryza sat AC104433 Oryza sat AC104433 Oryza sat AP0044117 Oryza sat AP004413 Oryza sat AP0044045 Oryza sat AP004169 Oryza sat AP004169 Oryza sat AP004169 Oryza sat AP004164 Oryza sat AP0049946 Oryza sat AP0049946 Oryza sat AP0049946 Oryza sat AP004991 Oryza sat AP004994 Oryza sat AP004994 Oryza sat AP004994 Oryza sat AP004994 Oryza sat AP00400000 Oryza sat AP003262 Oryza sat AP003636 Oryza sat AP003620 Oryza sat

AP004764 Oryza sat AP005459 Oryza sat AL662957 Oryza sat AC093088 Oryza sat

<pre>Xim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahl,B., Jin,S., Koo,H., Zismann,V., Hslao,J., Blunt,S., Vanaken,S., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C. Gryza sativa ssp. japonica cv. Nipponbare OSJNBa0059606 BAC genomic sequence Upublished 2 (bases 1 to 145999) Buell,R. Direct Submission Direct Submission Submitted (22-SEP-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA 3 (bases 1 to 145999)</pre>	d (08- center Center 2002 7 2002 This i ts of the of gaps led by equenc equenc finis	* 4003 71267: Cortig of 67267 * 71268 71367: gap of unknown * 71368 94679: Cortig of 233167 * 94780 122220: Cortig of 237441 * 122221 122320: gap of unknown * 122321 122320: gap of unknown * 122321 145999: Cortig of 23679 Location/Qualifiers Location/Qualifiers //Organism="Oryza sativa" //Chromosome="1" //Chromosome="1" //Chromosome="1"	/note="japonica cultivar-group" 40847 a 32003 c 31335 g 41412 t 402	Match 100.0%; Score 5001; DB 2; Length 145999; social Similarity 100.0%; Pred. No. 0; ss 5001; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AGGGAACACTACACTTTCCATCATGAAAAGTGTAACACACTAATGGTCATCCGTACTCAT 60	TGAATATGATGAAGTTGTACTGGGCTAAATTGGAAATTTAATTATACCAAGCCAATTCA 120 	ATAATCATAAGAATGAGTGCTCCATGAAACTAAATAAGAAAGTAGAACATAAGGTGCGT 180 	agicicitagciaitaicigataaaagaaaacaacacagagagaciagaga 240	GTACCATAGTTCAAATAGGCTTGAGCCAACATATGTCCAAGCTGGACCTTGGGCTTGGGTG 300	CTAAGGTGCAGATGGCCATCTTCTAGTGGCAAACCCTTTGCATCAACAAATCTCACGTTT 360
TITLE JOURNAL JOURNAL AUTHORS TITLE JOURNAL REFERENCE	TITLE JOURNAL MMENT	FEATURES	COUNT	Query Match Best Local Matches 500	1 A   81119 A	61 T   81059 T	121 A     80999	181 A   	241 G   	301 C
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416	1 TICACCGATICC	CAACAGCIACAIAAACCICGIIAGAGICCACAIGCCCAIIGANGIGGGGI 27 	2760 78360
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23	11 GGAGGAGCAAAG1 	'GGACGACGGAGAGAATGAGTCGGAGAGGAAGAAAGAGGAGAAACAGA 29 	
17.9	41 TATGGAGAATAA              79 TATGGAGAATAA	raggaairaartctagggtgtttgttgttaagttgtarccattctacgg 30( 	3000 78120
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7 6	21 ACCATTGTCGT/ 	augaagagaagaaataggatgaatgatgagatgagataaaaatatggga 31 	3180 77940
H 6	81 AAATTGGTTCC?                39 AAATTGGTTCC?	ATACCATCGAAAGTTCCTGAGTTTTGCTTTATACCATCGAAAATTTGTG 32	
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~ m	61 TGCCCTTCCTT               59 TGCCCTTCCTT	CACTCATCTAAATCTGGCCCAAATTTTCTCGTTTTTTCCTCTTTGGCTG 34	
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4 9	81 GGAGGAACATTG 	FIGAATAGAGGACTGCACGAGCACCGGAGCACGGCGAGTGACGAG 35	
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AC104433 207376 bp DNA linear HTG 02-APR-2002 Oryza sativa chromosome 3 clone OJ1754_E06, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.
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Direct Submission
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Direct Submitted (11-DEC-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 207376)
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* NOTE: This is a "working traft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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AC104433 207376 bp DNA linear HTG 02-APR-2002 Oryza sativa chromosome 3 clone OJ1754_E06, *** SEQUENCING IN PROGRESS ***, 34 unordered pieces.
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1 (bases 1 to 207376)
Buell,C.R., Yann,C., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II.L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.
Oryza sativa ssp. japonica cv. Nipponbare OJ1754_E06 BAC genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-DEC-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 207376)
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Submitted (02-ARR-2002) The Institute for Genomic Research, 971
Medical Center Dr. Rockville, MD 20850, USA
MAT 5, 2002 this sequence version replaced gi:18767486.
NOTE: This is a "working draft' sequence. It currently
consists of 34 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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gap of unknown length
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HTG 21-MAR-2002
clone
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Direct Submission
Submitted (29-AUG-201) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-12, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakieilas.affrc.go.jp, VRL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7444, Fax:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 167706 ACAATGGAATTATTTTGGCATGTCTACCTGACGGAATGTGATGGTATGTTATATAATA 167765
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OJ1134_F06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP004117
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                    167226 CTAAGGTGCAGATGGCCATCTTCTAGTGGCAAACCCTTTGCATCAACAAAATCTCAGTGTTTT
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                                                                                                421 GCTAGTCCTACCTGAAACACCACAAACAGGAATGGGGATTGCCTACTGTATTATGTGATA
                                                                                                                                                                                                                                      481 TAGCAGCGAAGAGTCTAATTTACAAGCGATTTGACGAATACCACAAATAGTTTTGTCTTG
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:0J1134_F06
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2 (bases 1 to 131487)
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Pred. No. 3.8e-146;
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Best Local Similarity 79.0
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combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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26762 c 26756 g 39195 t
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Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (2-1-2), Tsukuba, Ibaraki 305-8602, Japan (2-1-2), Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakiknias.affrc.go.jp, WL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

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1; Poales; Poaceae;
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                                                                  --- ATGCGTCGGGACCCGAGACAAGG 44977
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3884 CGATGCTTGGTGAAGAAGATGCTGCTTTTGATCTGGATGCGTCGGGGGACCGGAGAAGG 3943
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0459E03
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Bukaryota, Viridiplantea; Streptophyta; Em
Spermatophyta; Magnoliophyta; Lillopsida;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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/db_xref="taxon:39947"
/chromosome="6"
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1. .159290
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HTG 05-JUL-2002
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OSJUBBA0049101, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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clone:OSJNBa0049101.
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                                                                                                                                                        2351 ACCTAGGTGTCTGGGCACCAAGCCTGATACTTGTGGTTATCGGCTGTGATTTTCTGACGT 2410
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                 ||||| || GACCAACTATGCATTGTCCGTTGGTGCCCCTGACCTCATCCCCCTTTCCCTGAC
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Oryza sativa (japonica cultivar-group)
Bukaryota; Vitidiplantas; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
                                                                                                                   50;
                                                                          Length 96360;
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                         200 others
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Pred. No. 1.1e-33;
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   /clone="OJ1111_B02"
21675 c 21926 g
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The nucleotide sequence of this BAC clone was generated by compining Monsanto and Rep-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are perseated as runs of N. The order of the pieces is believed to be correct as given, The order of the pieces is believed to be correct as given, nowever the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                            26724 ATAATCAAGCAAATTGAAATCTACTCTTCCT----CCCTACTCGTAGTCAATTTATAC 26670
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                                                                              1803 ITGGGACAAATAATTTGAAATCTACTCCTCCTCACTACTTCTACTCGTAGTCAATTTATAA 1862
                                                        GIGGGACCCCACCACCCCCCCCCCCCCCCATGTTCGACTGCCCCCCAGGATGAACAC 1682
                                                                                                                                     Oryza sativa (japonica cultivar-group) chromosome 8 clone
OJ1111_B02, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
AP003867
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:OA1111_BA0
Published Only in Database (2001)
2 (bases 1 to 96360)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
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Submitted (13-FEB-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-2, Tsukuba, Ibaraki 305-6602, Japan 12-1-3, Tsukuba, Ibaraki 305-6602, Japan 12-1-308-38-7441, Fax:al-299-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are peptesented as runs of N. The order of the pieces is believed to.be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                               AP004759 127498 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone P0670E08, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lilliopsida; Poales; Poaceae;
     -----AGTTGGGGGGAGGGAGCTAGGTGGAGGATGGAGAATGAGTTTGAGAAAGG 134246
                                                                                       Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:P0670E08.
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/cultivar="Nipponbare"
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                                                          AAGAGGAGAAACAGATATGGAGAATAA--GAAATAAATCTAGGGTGTTTGTTGTTAAGTT
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8,
clone:P0670E08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29255 c 28860 g 34022 t
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2 (bases 1 to 127498)
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                                                                                                                               Direct Submission
Submitted (04-UIL-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (B-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:R1-298-89-7441, Fax:R1-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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/cultivar="Nipponbare"
     BAC
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
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Pred. No. 1.2e-33;
0; Mismatches 160; Indels
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                                                                                                        Sasaki, T., Matsumoto, T. and Katayose, Y.
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35902 a 31425 c 31045 g 36057 t
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are represented as runs of N. The order of the pieces
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64.7%; Pred. No. 1.8e-28;
ive 0; Mismatches 192;
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a 32003 c 31335 g 41412 t
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/organism="Oryza sativa"
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Matches 385; Conservative
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1 (basea 1 to 14599)
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,Y., Hsiao,J., Bulut,S., Yanaken,S., Utterbach,T., Feldblyum,T., Mang,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.

Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0059G06 BAC genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145999 bp DNA linear HTG 08-MAY-2002 Oryza sativa chromosome 3 clone OSJNBa0059G06, *** SEQUENCING IN AC096690
                                                                                                                                                                                                                                                    77490 -----AGTTGGGGGAGGAGGAGGAGGAGGAGGAGGAGAAAGG 77542
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                                77201 GACCAACTATGCATTACCATTGTCCGTTGGTGCCCCTGACCTCATCCCCTTTCCCTGAC 77260
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             2514 AGTACAATGTAACAACCTCGAGACCTCCATGAACTCCGAGATTGCCCTCACACGAGAAC 2573
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                                                                                                                                                          2627 GTCCTCCTCTTGTCCCTCCCCAGCCACGACAAAGGTGACCTCGCTGTCGCAGTTACCT 2686
                                                                                                                                                                                                                                   2687 ITCIACTIGCCGAITICACCGAITCCAACAGCIACAIAACCICGTIAGAGTCCACAIGCC 2746
                                                                                                                                                                                                                                                                                                           CATTGATGTGGTGTGGGGAAGGGGAAAGAGGATGTGGGGATGTCATC-GTGTTGGGGATGA 2805
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On May 8, 2002 this sequence version replaced gi:19881803.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
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Direct Submission
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75694 ACCTGGATCACCAGCTCCGGCAACGCCAGGTCTCGCCGGACGTCGCGCACCATGCCC 75753
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* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
the accession number will be preserved.

* 3902: contig of 3902 bp in length

* 4003 71267: contig of 67265 bp in length

* 71268 71367: gap of unknown length

* 71368 71367: contig of 23312 bp in length

* 94680 94779: gap of unknown length

* 12221 122320: contig of 23679 bp in length

* 12221 122320: gap of unknown length

* Location/Qualifiers
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2 (bases 1 to 176224)
                                  176224 bp
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HTG; HTGS_PHASE2.
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es 240; Conservative (
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Submitted (05-SEP-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-289-87-441, Fax:81-299-387-468)

Tiel:18-289-387-441, Fax:81-299-387-468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 configs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1. 121752
               APO04130 121752 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultivar-group) chromosome 8 clone OJ1014_B05, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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                                                                                                                                        Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:011014_B05.
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
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/cultivar="Nipponbare"
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:0J1014_B05
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Pred. No. 2.5e-28;
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2 (bases 1 to 121752)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
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Submitted (1976712009) land) land)
Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:itsaasakieniasa.affro.go.jp, WEL:http://rgp.dna.affro.go.jp/, Tel:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.
HTG 17-MAY-2002
                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaes; Oryza.
                               Oryza sativa (japonica cultivar-group) chromosome 8 clone
OSJWBa0053M06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:OSJNBaC053MO6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46774 TACTACTCCCTCCGTTCCAAAATAAGTGTAGTTTTAGCACTGTTCATGTTCAAGGTTTGA 46833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46954 ATAAGACGGATGGTCAAAGCGCTAAACACGGATATCTATGGCTGCACTTATTTGGGACG 47013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4131 TAGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACGTTTGA 4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4251 ACATGAATAGTACTTTATGTGTGACTAATTTTTTTTAATATTTTTTATTATTTTTCAA 4310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4311 ATAAGACGGATGGTCAAAGCGCTAAACATGGATATCTATGGCTACACTTATTTTGGGACG 4370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-MAY-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
clone:0SJNBa0053M06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 others
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Pred. No. 2.5e-28;
3; Mismatches 15; Indels
   linear
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   DNA
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RESULT 12

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/translation-"MVYAMIDSIRLINKYQKRHDKQVQRNFRILDITEMIDIIKVIRM
KNIVKVISLILIGVGLLLINSTSVGSICVCKYFKEKTHPAYKETHLRPIRRKYTDWRA
HKSODTAFEWYITVITALIKANGSVSLFKERLGDLSEVDGRLSNKPNMLEKLNIADLHO
WINAVHIETTRINYIELIKGKRIFVSG"
join(24567. 24773,24885. 25163,25427. 25524,25675. 25882)
/gene="Billieli.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(24567. .24773,24885. .25163,25427. .25524,25675. .25882)
/gene="B1111E11.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKTWASRTLREFAAPSADNVATRLOFLZICSTYTIKGYNLDAVRLRLFLFSLLGRAKO
WFYINRVAVNIWDKCSTAFLSKFFPMGKINALRGRISSFQTRDESIPBAWERLOEUG
KKTIEESRAGGIYRETRNMTRNERESSSSSTPVQMSSGVPPSPSEGWRSSSSRWDLSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mplfcikkvkkkonmipghigyigcvpgknslrdshggelpsina
nigtrgcdvfdrngkagkmpkhdpwtywsmlrafyakthfviraanfcgliatlaheg
amffdrnekvgkapkgdfwtywsvkertafrtpgddreprpenlrndrsyakhtskat
            /translation="MTSPPAVARARKIASERRRDDANGGHQHINGRRRRGRNGGHLR
.DDDGGAPATYGDGGGYDEIGDGLVTTTATSPSNDDDRIDGGARLKIRRRRRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MEDHTRKLONKADIASAEVHKSGGWGTDEQAVIGYLAHRDATQR
KQIRLTYEENYNENLIQRLQSELSGDLERAMYHWYLDPVERQAVMVNTATKCIHEDYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNDALAKSBAKILHETVTNGDTDHGELIRIVGTRSRAQLNATFSWFRDERGTSITKLH
APRFDHQALQHGADPTGYSHALRTALRCISDANKYFVKVLRNAMHKSGTNEDSLTRVI
                                                                                                                                                                                             complement(join(14589. 14792,14904. 15023,15078. 15290,
15389. 15607,15720. 15865,16296. 16365))
/gene="BlllIEll.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIVEIACTNSSSELLAVKRTYHVLYKCSLEEDVAARATGNLRSLLLALVSTYRYDGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(17303. 17441,21169. 21190,21797. .22025,
22151. .22324))
/gene="B1111E11.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTGFNLSENFKENPEAFFRSVRPRVVAPKKSLPIEKLAIPVPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLHAEKDLKGIKDAPOKRASVALEKAIGNDTSGDYKSFLMALLGSGI"
complement(join(17303. .17441,21169. .21190,21797. .22025,
                                                                                                                                 .15023,15078. .15290,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="hypothetical protein
similar to Oryza sativa chromosome10,0SJNBb0089F16.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="probably inactive due to stop codon(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein similar to Oryza sativa chromosome3,OSJNBa0026A15.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [RRMDTLDIQIGEIQYNLTEHVAQTQEWQQSADAQFANINDMMQQ"
                                                                                                                        complement(join(14589, .14792,14904, .15023,
15389, .15607,15720, .15865,16296, .16365))
/gene="B1111E11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="BlillEll.7"
join(35262. .35643,43596. .43702)
/gene="BlillEll.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(44530. 44843,44934. 45375)
/gene="Bl111E11.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            loin(35262. .35643,43596. .43702)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="hypothetical protein"
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/gene="B1111E11.8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAC0330.1"
/db_xref="G1:21743337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAC03329.1"
/db_xref="G1;21743336"
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                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAC03328.1"
                                                                     complement(8839. .9352)
                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:21743335"
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/gene="B1111E11.6"
30135. .32223
/gene="B1111E11.6"
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/qene="B1111E11.4"
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                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03°CCT-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-12, Tsukuda, Labraki 30°-8602, Japan 12-12, Tsukuda, Labraki 30°-8602, Japan 12-12, Tsukuda, Labraki 30°-8602, Japan 12-130-308-38-7468)

(B-mail:tsasaki@mias.affrc.go.jp, VEL.http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jul 12, 2002 this sequence version replaced gi:17026098

Genes were predicted from the integrated results of the following: GENSCANI.0, ELASTRY.0, BLASTRY.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCEN NonRedundant Protein database. In recognize the following: GENSCANI.0, Labrath.000-138-7403 and the CDNA sequence database at RGP. Protein homologies of the coding regions were searched against the identified cDNA sequences using BLASTR.0.0 with the corresponding DDBJ accession no. and RGP Clone ID.

A gene with identity or significant homology to a protein is classified as an annew, putative- and "like protein." A gene without significant homology to any protein but with BST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orienterion of the sequence of Blillill clone has an overlap with B1080D07 (DDBJ:AF003203) at the position 146,696 to 152,835 of 3' end. Detailed information of verlap and assembly quality together with the procession of this entry is available at hittp://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                     PLN 13-JUL-2002
                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
         aruo4224
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
BAC, clone:B1111E11.
                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:B1111F11.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sasaki,T., Matsumoto,T. and Yemanoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:B1111E11
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/cultivar="Nipponare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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join(8253. 8336,8386. 8595)

/gene="B1111E11.2"
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/db_xref="G1:21743334"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Only in Database (2001)
2 (bases 1 to 152835)
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/gene="B1111E11.1"
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                                                                                                                                                                                                                                                                                                                                                                     Ehrhartoideae; Oryzeae; Oryza.
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/note="3' LTR"
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                                                        DEFINITION
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Agrobiological Sciences, Race Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:Eseaskiénisas afrec go.jp, WEListtp://rgp.dna.affrc.go.jp, Pramail:Eseaskiénisas afrec go.jp, WEListtp://rgp.dna.affrc.go.jp/, Tel.81-298-38-7469)

The nucleotide sequence of this BAC clone was generated by combining Morsanic and RGP-Japan sequencing data.

WOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the gaps between them to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* WOTE: This is a "working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                      HTG 23-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA, clone:011311_D08.
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                                                                                                                                                                                                                                   AP004849 163704 bp DNA linear HTG 23-MAR
Oryza sativa (japonica cultivar-group) chromosome 2 clone
OJ1311_D08, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:0J1311_D08

    163704
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                     4369 CGGAGGTAGTAGGCTATAAACCAGCTATAAACATATTTTAAAAGAGATAAAA 4419
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Pred. No. 6.3e-26;
0; Mismatches 19;
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35204 c 34892 g 46875 t
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2 (bases 1 to 163704)
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HTG; HTGS_PHASE2
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63077. .63182.63282. .63374,63454. .63349,64125. .64847,
64968. .65116,66390. .66476,66497. .66581)
/gane="Billill.12"
                                                                                                                                                                                                                                                                                                                                                                                   /translation-midgenipenekeypergyrprayapoktlphekpalpappi
FWTMASKTLREFAAPSTDNVALGPQINIGDMDFDLKSSLITMAQASPECGKPNVDANA
HLQOPLECCSTTIKGYSBDAIRLENEPFSLLGRAKQWFYANRAAVNWURCSPGFLS
complement(43388. 448579)
/gene="Blilleli.10"
/gene="Blilleli.10"
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GWAFYSDDDDEHRRAGSGGEARPRATILPLEKTRRWMGREADRGADRGNEGTGE
WRSGODATGHRWHATLAGGEARPRATILDLEKTRRWMGREADRGNEGTGE
WPSGODATGHRWHATLAGGELRAKRRRRRWMGREADGAGGWPA
PREKEEDGGDATGHRWHATLAGGELRAKRRRRWMG
PREKEEDGGDVSHRTGRAGGERPW
FYAGVGAGVPDWGHESRRKRLGGERREBEGWGINSP"
COMPLEMENT (46012. 44653)
/gene="Billibil.9"
/gene="Billibil.9"
/foote="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAC0334.1"
/db_xref="G1:2174334.1"
/translation="MLRALPERYETLVTMLINSDMSRWTPASLLGKINTNDMYKLKKK
EMEEASPSKPKLKIRARAK"
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join(60720. .61097,61272. .61421,62316. .62685,62854. .62
63077. .63182,63282. .63374,63454. .63549,64125. .64847,
64968. .65116,66590. .66476,66497. .66581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similar to Arabidopsis thaliana chromosome 3, At3g54500"
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                                                                                                                                                                                                                                                                                                         similar to Oryza sativa chromosome10,0SJNBb6089F16.9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAC03335.1"
/db_xref="G1:21743342"
                 /protein_id="BAC03332.1"
/db_xref="G1:21743339"
                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAC03333.1"
/db_xref="GI:21743340"
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/note="5' LTR"
55770. 57616
/gene="Bll11E11.11"
/gene="Bll11E11.11"
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Parail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Parail:tessaskiehisas.affro.go.jp, WEL;http://rgp.dna.affro.go.jp/, Tel:81-298-38-7468)
The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced as soon as it is available and the accession number will be preserved.

* The accession number will be preserved.
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1; Poales; Poaceae;
  Db 113730 ATAAGACGGATGGTCAAAGCGCTAAATACGGATATTTATGGCTGCACTTATTTGGGACG 113789
                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1147_D11.
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                                                                                                                                                                                                                                                                                      Oryza sativa (japonica cultivar-group) chromosome 6 clone
OJ1147_D11, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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Published OBLy in Database (2001)
2 (bases 1 to 138906)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Bubniston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-JUL-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
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                                                                                                                                                                                                                                                                   linear
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Eukaryota, Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                   DNA
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39967 a 29996 c 29997 g 38791 t
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1. .138906
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Matches 240; Conservative
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                                                                                                                                                                                                                                                           nollows 126637 bp DNA linear HTG 23-APR-2002 Organ sativa chromosome 3 clone 031263H11, *** SEQUENCING IN PROGRESS ***, 3 ordered pieces.
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Wing,R.A., Tu.Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R. and Simmons,J.
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4309 AAATAAGACGGATGGTCAAAGCGCTAAACATGGATATCTATGGCTACACTTATTTGGGA 4368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-APR-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

The accession number will be preserved.

The gap of unknown length
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/organism="Oryza sativa"
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QY 4297 TATTAATTTTCAAATAAGACGGATGGTCAAAGCCCTAAACAGGATATCTAIGGCTACA 4356
Db 11717 TATAAATTTTACAAATAAGACGGATGGTCAAAATGCTAAAACACGAATATCTAIGGCTACA 11776
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Oy 4357 CTRATTTGGGAGGGAGGTAGTA 4379
Db 11777 CTTATTTGGGACGGAGGTAGTA 11799

Search completed: March 26, 2003, 16:07:03 Job time : 16632.4 secs

Arabidopsis thalia

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March 25, 2003, 18:27:39 ; Search time 762.288 Seconds (without alignments) 14774.266 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Rice Ditto-Osl mic	Rice Ditto-Osl nuc	Nucleotide sequenc	Rice Ditto-Osl nuc	Nucleotide sequenc	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia
SUMMARIES	ABI,49988	ABL49989	AAZ61434	ABL49987	AAZ61433	AAC48061	ABN98574	AAC45528	AAC46278
DB	24	24	21	24	21	21	24	21	21
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                                                                                               Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction fragment length polymorphism applicable in cell genetics e.g. for analysing and selecting specific breeds of plants. The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable identification of the site and isolation of the required gene.

ABLA9926 to ABLS0036 represent nucleotide sequences used in the exemplification of the present invention.
                                                           detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it.
                                                 present invention describes a method for constructing a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                    4495 IGACAAGTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTA 4554
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                                                                                                                                                                                                                                                                 2.8%; Score 139.8; DB 24; Length 561; ilarity 75.9%; Pred. No. 4e-20; Conservative 0; Mismatches 57; Indels 2;
                                                                                                                                                                                                                                                                                          57; Indels
fragment length polymorphism applicable in cell genetics
                                                                                                                                                                                                                                        Sequence 561 BP; 191 A; 76 C; 87 G; 207 T; 0 other;
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0; Mismatches
                       Example 4; Fig 17; 110pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NISB ) JAPAN TOBACCO INC. (SYGN ) SYNGENTA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komori T, Nitta N;
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4615 TCTCA 4619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 TTTTA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
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                                                                                                                                                                                                                                                                                         Matches 186;
                                                                                                                                                                                                                                                                  Query Match
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detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it. Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction fragment length polymorphism applicable in cell genetics e.g. for analysing and selecting specific breeds of plants. The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable dientification of the site and isolation of the required gene.

ABLA9926 to ABL50036 represent nucleotide sequences used in the
Construction of marker for detecting plant genome polymorphism with use of transposable element, useful particularly in studying restriction fragment length polymorphism applicable in cell genetics
                                                                                                                                                    The present invention describes a method for constructing a marker for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4435 CAGCGGACTATATATTTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATA 4494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 CAGGGGCTACAGATCTGTAGTCAGCTGCAGCACGGACTCCAATACGTAATGTATG--TA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disease resistance protein; rice; variety Tsuyuake; Pi-ta gene; resistance gene; Pi-ta resistance gene-mediated defence response; fungal pathogen; rice blast fungus; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 561;
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/transl_except= (pos: 1118..1121, aa: Gln)
/note= "contains an intron"
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0; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 561 BP; 191 A; 76 C; 87 G; 207 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%; Score 139.8; 75.9%; Pred. No. 4e-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exemplification of the present invention.
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                                                                                               Example 4; Fig 17; 110pp; Japanese.
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Matches 186; Conservative
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The present invention describes a method for constructing a marker for detecting polymorphisms in a plant genome. The method comprises the production of a primer for nucleic acid amplification by using the base sequences of a transposable element and/or the domain adjacent to it.

Also described is a marker for detection polymorphisms in plant genomes. The constructed marker can be used for detecting plant genome.

The constructed marker can be used for detecting plant genome polymorphisms, which is useful particularly in studying restriction fragment length polymorphism applicable in cell genetics e.g. for madysing and selecting specific breeds of plants: The method is simple, easy, less time consuming and not so laborious, e.g. in the study of less frequently occurring polymorphism between various species to enable the dentification of the site and isolation of the required gene.

Alsi49926 to Abl50036 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4385 TABACCAGCTATABACATATTTBAAGAGATAAAAGAAGAGAGAATAGCAGCGGACTA 4444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Construction of marker for detecting plant genome polymorphism with u of transposable element, useful particularly in studying restriction fragment length polymorphism applicable in cell genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rice; plant; detection; polymorphism; transposable element; genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 AGATGATTTTAAGTTAGTAGTGGGCTATACTATTAAACTTGCTCTAATTGTTTTA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of the genomic clone of the Pi-Ta gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 544 BP; 179 A; 72 C; 91 G; 202 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Fig 17; 110pp; Japanese
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Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-241759/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Komori T, Nitta N;
                                                                                                                                                                    WO200212484-A1
                                                                                                 Oryza sativa.
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                                      dene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid fragments conferring Pi-ta resistance gene-mediated defence response for producing transgenic plants resistant to fungal pathogens, especially rice blast fungus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2690 CAGCAGCCTACAGATCTGTAGCCAGCTGCAGCACTCTAAGACGTAATGTGTG-TA 2747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4435 CAGCGGACTATATTTTTTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATA 4494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes a disease resistance protein of rice variety rsuyuake. The rice Pi-ta gene was cloned by a map-based cloning strategy. The Pi-ta protein has a novel structure, compared to all known classes of resistance gene products. The polynucleotide sequence confers a Pi-ta resistance gene-mediated defence response against diseases caused by fungal pathogens, particularly the rice blast fungus. Introduction of the cloned Pi-ta gene into susceptible rice confers resistance to pathogen strains.
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                        /number= 1
1592..3056
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/*tag= d
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Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valent BS, Bryan GT;
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                                                                                                                                                                                                                                                                                              WO200008162-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1998;
21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3319 CAGCTGCAGGACTCTAAGACGTAATGTGTG--TATGACAGGTAGGACCAAGTATA 3376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4397 AAACATATTTTAAAGAGATAAAAGAGAGAGAGAAATAGCAGGGGGCTATATATTTGTAGC 4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4457 CAGCTACAGCACGGACTCAAAGACGTAATGTGTATATGACAAGTAGGACCAGGTATTA 4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes a disease resistance protein of rice variety Yashiro-mochi. The rice Pi-ta gene was cloned by a map-based cloning strategy. The Pi-ta protein has a novel structure, compared to all known classes of resistance gene products. The polynucleotide sequence confers a Pi-ta resistance gene-mediated defence response against diseases caused by fungal parhogens, particularly the rice blast fungus. Introduction of the cloned Pi-ta gene into susceptible rice confers resistance to pathogen strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
             Disease resistance protein; rice; variety Yashiro-mochi; Pi-ta gene; resistance gene; Pi-ta resistance gene-mediated defence response; fungal pathogen; rice blast fungus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 5757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4517 AGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAACTATGAT 4567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5757 BP; 1638 A; 1202 C; 1251 G; 1666 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%; Score 121.8; DB 21; Length 86.0%; Pred. No. 7.5e-16; tive 0; Mismatches 22; Indels
                                                                                                                                                              /rote= "contains 1 intron"
1256..2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                    Location/Qualifiers
1256..5505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 56-57; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       99WO-US17706.
                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0336946
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                                                                                                                                                                                                                                       /*tag= c
/number= 1
3664..5505
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valent BS, Bryan GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-205715/18.
P-PSDB; AAY69307.
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                                                                                                                                                                                                                                                                                                                             WO200008162-A1
                                                                           Oryza sativa.
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21-JUN-1999;
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PR 18-70N-1999; 9918-013946.

PR 18-70N-1999; 9918-013346.

PR 18-70N-1999; 9918-013346.

PR 22-70N-1999; 9918-013346.

PR 22-70N-1999; 9918-013375.

PR 22-70N-1999; 9918-013375.

PR 22-70N-1999; 9918-014035.

PR 23-70N-1999; 9918-014035.

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PR 02-70N-1999; 9918-014230.

PR 13-70N-1999; 9918-014230.

PR 11-70N-1999; 9918-01433.

PR 11-70N-1999; 9918-014432.

PR 11-70N-1999; 9918-014432.

PR 11-70N-1999; 9918-014432.

PR 11-70N-1999; 9918-014432.

PR 11-70N-1999; 9918-014433.

PR 12-70N-1999; 9918-014433.

PR 12-70N-1999; 9918-014433.

PR 12-70N-1999; 9918-014433.

PR 22-70N-1999; 9918-014433.

PR 22-7
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encoded protein, and mapping functional regions of protein
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                                                                                                                                                                                                                                       transgenic; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Arabidopsis thaliana nucleic acid for identifying homologous genes, producing compositions that modulate the expression or function of its
1421 CGCAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAG-----GAGGGCGTTAG 1474
                                                      1475 CGAAGGACATCCCGGGACCGACGCCGCAGGTGCGTTGGAGTCGATGCCGTTGTGGAGCG 1534
                                                                                     GCTCGTGGGCCTCCTCCTCCTATCGGAGCTGCGGGGAGGCGGAGGATGGAGGGGTTGGGGG 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raines TM, Yu Y;
,, Woessner JP, Haas WD;
Allen K, Hoffman N;
                                  2680 GGCACGGCACCAACCCGATCAGGTTTCCAGGCGATTCTTCACGGTTAG
                                                                                                                                                                                                                                     Arabidopsis thaliana; plant; insecticide; fungicide; transgenic
disease; crop; thale cress; tolerance factor; insect; pathogen;
                                                                                                                                                                                                                      Arabidopsis thaliana expressed polynucleotide SEQ ID NO 342.
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Ledford BL,
, Davis KR, A
                                                                                                                              2500 CGCATTCCGGTGGAAGGATTTTATCCCA 2473
                                                                                                                   1595 GGCACTCGGGGGGAACCATGCCGTCCCA 1622
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Page A, Mathew AV,
Kricker M, Slater T,
                                                                                                                                                                        ABN98574 standard; DNA; 949
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PAGE A.
MATHEW A V.
LEDFORD B L.
WOESSNER J P.
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HAMILTON C M.
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GARCIA C A.
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RAINES T M.
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ALLEN K.
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The invention relates to an Arabidopsis thaliana nucleic acid (I)

Comprising a sequence capable of hybridising under stringent conditions
to a sequence sclerced from any one 0 599 sequences (ABN98123-ABN99231),
given in the specification or its fragment. A polypeptide (II) encoded by
given in the specification or its fragment. A polypeptide (II) encoded by
(I), a transgenic plant (III) comprising an exogenous nucleic acid or a
genetically modified cell (IV) comprising an exogenous nucleic acid or a
genetically modified cell (IV) comprising an exogenous nucleic acid or a
useful in identifying homologous or related genes, in producing
compositions that modulate the expression or function of its encoded
protein, mapping functional regions of the protein and in studying
associated physiological pathways. (I) is also useful in
screening assays of various plant strains to determine the strains that
stress. (II) and (III) are useful for screening of biologically active
are best capable of withstanding a particular disease or environmental
stress. (II) and (III) are useful for screening of biologically active
gents, e.g. fungicides, inserticides, etc., for elucidating biochemical
crops to prevent or treat disease. (II) are also useful in screening
programs to identify agents that minto or enhance the action of tolerance
factors. Such agents are useful in improved methods of treating
characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chhance their tolerance to environmental stress. (I) is also useful confidential production of a biosynthetic product in a plant. (III) is useful for identifying other mediators that may induce expression of proteins of interest, for setablishing the extent to which any specific insect and/or pathogen is responsible for damage to a particular plant, for identifying other mediators that enhance or induce tolerance to environmental stress, for identifying factors involved in the insert productions of nutritional, commercial, or medicinal value and for identifying productions of nutritional, commercial or medicinal value. (IV) is useful in the study of genetic function and regulation, or alteration of the cellular metabolism and for screening compounds that may affect the biological function of the gene or gene products. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format gart of the printed specification, but was obtained in electronic format and regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTCTCCCCCCTGG 1302
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Claim 1; SEQ ID NO 342; 49pp + Sequence Listing; English.
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nes 191;
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llarity 55.8%; Pred. No. 1.9e
Conservative 0; Mismatches
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 Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 46825
     1597 CACTCCGGGGGAACCATGCCGTCCCA 1622
               820 CATICCGGTGGAAGGATTTTATCCCA 845
                                                         AAC45528 standard; DNA; 1024 BP
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99US-0138094
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                              1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGCTCTCGAGGGCGACCCTGGAGCGGCGGACG 1362
                                                                                                                                                                                                                                          ATCCTCTCGTACAAGTGGCTTCCACGCTCCACTTTTATCGCCGTTCCACGGAAGCG 469
    1363 AGATCGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG
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990S-0149722.
990S-0149723.
990S-0149929.
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990S-0150566.
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9905-0153070
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0; Mismatches 191; Indels 6;
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99US-0123180.
99US-0123548.
                                                                                                  tch 2.4%;
al Similarity 55.8%;
249; Conservative 0
        99US-0161405.
99US-0161406.
99US-0161369.
99US-0161361.
99US-0161361.
99US-0161923.
99US-0161993.
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99US-0161404
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05-MAR-1999;
09-MAR-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
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                                                                                                   Query Match
Best Local 9
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AAC47620/c
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RR 16-70L-1999; 990S-0144086.

RR 16-70L-1999; 990S-0144086.

RR 19-70L-1999; 990S-014431.

RR 19-70L-1999; 990S-014431.

RR 19-70L-1999; 990S-0144332.

RR 19-70L-1999; 990S-0144332.

RR 21-70L-1999; 990S-0144332.

RR 22-70L-1999; 990S-0144332.

RR 22-70L-1999; 990S-0144332.

RR 22-70L-1999; 990S-0144332.

RR 22-70L-1999; 990S-0145088.

RR 22-70L-1999; 990S-0145088.

RR 22-70L-1999; 990S-014508.

RR 22-70L-1999; 990S-014708.

RR 13-70C-1999; 990S-014708.

RR 13-70C-1999; 990S-014708.

RR 13-70C-1999; 990S-014708.

RR 13-70C-1999; 990S-014308.

RR 13-70C-1999; 990S-014308.

RR 22-70C-1999; 990S-014309.

RR 23-70C-1999; 990S-01430
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2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 118.4; DB 21; Length 3187; Pred. No. 3.1e-15; 0; Mismatches 191; Indels 6;
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AAC41895/c
ID AAC41895 standard; DNA; 1024 BP.
XX
9905-0158029
9905-0158329
9905-0159329
9905-0159294
9905-0159295
9905-0159329
9905-0159330
9905-0159331
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9905-0159637
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9905-0160740
9905-0160760
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ilarity 55.8%;
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Best Local Simi
Matches 249;
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99US-0150566.
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99US-0149722.
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18 - JUN - 1999;
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29 - JUN - 1999;
30 - JUN - 1999;
01 - JUN - 1999;
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04-AUG-1999

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28-JUL-1999;
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23-AUG-1999;
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25-AUG-1999
     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                             Arabidopsis thaliana DNA fragment SEQ ID NO: 33532
                                                                                                                                                                                                                 9905-0121825.
99078-0123180.
99078-0123180.
99078-0125788.
99078-0125788.
99078-0125784.
99078-0127462.
99078-0127462.
99078-0128714.
99078-0128714.
99078-0137848.
99078-0137481.
99078-013481.
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990S-0139492.
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990S-0139459.
990S-0139460.
990S-0139461.
990S-0139462.
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99US-0138540.
99US-0138847.
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                        (first entry)
                                                                                                                     Arabidopsis thaliana
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14-MAY-1999;
14-MAY-1999;
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18-MAY-1999;
20-MAY-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
29-MAR-1999;
01-APR-1999;
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23-APR-1999;
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24 - MAX - 1999)
25 - MAX - 1999)
27 - MAX - 1999)
28 - MAX - 1999;
01 - JUN - 1999;
04 - JUN - 1999;
07 - JUN - 1999;
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30-APR-1999;
30-APR-1999;
04-MAY-1999;
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07-MAY-1999;
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16-JUN-1999;
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AAC41895;
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AAA/9263 to AAA/9736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from encalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis; Pinus radiata; Monterey Pine; Plant; modification; Plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism; ss.
                                                                                                                                         1537 TCGTGGGCCTCCTCCTATCGGAGCTGCGGGAGAGGCGGAGGGGATGGAGGGGTTGGGGGC 1596
1423 CAGGGGACGAGGCCGATGACAGGGAA-----CTGGCCGGAGGGAAGGAGGGCGTTAGCG 1476
                                                                     1477 AAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGC 1536
                                 468 CACGGCACCAACCCGATCACAGCCGAATCTGTTTCCACGCGATTCTTCACCGCGTTAGCG 409
                                                                                                                                                              Pinus radiata cell signalling involved polynucleotide SEQ ID NO:374.
                                                                                              408 AACGCCATTCCTGGACCTACTCCACACTTTACCTGTGTCAATGTCAACGTGTAGTGGC
                                                                                                                                                                                                               1597 CACTCCGGGGGAACCATGCCGTCCCAG 1623
                                                                                                                                                                                                                                      288 CATTCCGGTGGGAGGATTTATCCCAG 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 176; 527pp; English.
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                                                                                                                                                                                                                                                                                                                                        AAA79573 standard; cDNA; 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000; 2000WO-US00724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0228986.
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Pred. No. 2.7e-15;
0; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                       9908-0157865.
9908-0158029
9908-0158369.
9908-0158369.
9908-0159294.
9908-0159294.
9908-0159331.
9908-0159331.
9908-0159331.
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990S-0154779.
990S-0155486.
990S-0155659.
990S-0156458.
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99US-0160814.
99US-0160815.
99US-0160980.
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99US-0161405.
99US-0161406.
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99US-0162142
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99US-0160989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 55.7
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
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25-OCT-1999;
25-OCT-1999;
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05-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                       06-0CT-1999;
07-0CT-1999;
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22-OCT-1999;
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07-SEP-1999;
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                                                                                                                                             10-SEP-1999;
                                                                                                                                                                           15-SEP-1999;
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22-0CT-19
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Gaps

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Indels

37;

DB 20; Length 2380;

1267

PDC; rice;

SS

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The invention relates to an isolated hypoxia inducible promoter (HIP) obtained from the pyruvate decarboxylase (PDC) gene in rice. The HIP can be used for regulating the expression of foreign genes in cells such that the genes are expressed upon exposure of the cells to anaerobic conditions. The HIP can be used to produce transgenic plants that are more tolerant to fanaerobic conditions, e.g. flooding. The HIP can also be used to enhance the expression of gene products that are normally induced under hypoxia conditions. The promoter can be operably linked to genes that express a protein product that is effective against solid tumours sequence obtained from rice pdc2 gene.
                                                                                                                                                                                                                                                                                                                          4441 ACTATATATTTGTAGCCAGCTACAGCACGCACTCAAAGACGTAATGTGTGTATATGACAA 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGGACCAGGTATTAAGAGTATAGTAAGCAACTATTGTATGAATTAGCTATTACATTAA 4560
                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated hypoxia inducible promoter (HIP)
                                                                                                                                                                                                                                                                                                                                                                                                     Hypoxia inducible promoter; HIP; pyruvate decarboxylase;
gene expression; transgenic plant; anti-tumour agent; ss.
                                                                                                                                                                                                                                  Sequence 2380 BP; 759 A; 533 C; 425 G; 663 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice pyruvate decarboxylase (pdc2) gene sequence
                                                                                                                                                                                                                                                             Score 107.8; DB 2
Pred. No. 5.2e-13;
                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated hypoxia inducible promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Examples; Page 5-8; 38pp; English.
                   Claim 2; Page 4-5; 38pp; English.
                                                                                                                                                                                                                                                               2.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX31999 standard; DNA; 5526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US18955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                             Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PURD ) PURDUE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-229236/19.
                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY03900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JUN-1999
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                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX31999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
AAX31999/c
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                                                                                                                                                                                                               1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGCCGGCGACCCTGGAGCGGCGGCGACC 1362
                                                                                                                                                                                                                                                                        1363 AGAICGGAGTAGAGGICGGIGCCCTIGGCCCAGICGGCCAICCIGGIGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                     1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGA------AGGAGGGCGTTA 1473
                                                                                                                                                                                                                                                                                                                                                                                                 1474 GCGAAGGACATCCCGGGACCGACGCCGCAGGTGCGTTGGAGTCGATGCCGTTGTGGAGC 1533
                                                                                         1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGCCCAGCGCACGGTGTCGCTCTCCCCCCTGG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGCACTCCGGGGGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCCGCGCCCCGCGC 1653
                                                                                                                   546 ACCTGGATGAAAGGAGATCGGGATGTTTCAGATCAGAGCGGATATCATGGATAAGTCTC 487
                                                                                                                                                                           486 TCGAGATTAIGTTTATAGCTATTAGCATTCTTCTCAGATTCTGTATCACTTTCGCCTTGA 427
                                                                                                                                                                                                                                                                                                                                                               306 CAGGGAACTAAACCAATACGAGCTTTTTTGGGATCTTTATAATGCTTCAGTATAGTGTTT 247
                                                                                                                                                                                                                                                                                                                                                                                                                         246 GCAAATATCATTCCAGGACCTACTCCACACTTTGTTTATCTATATCGCCATGCAAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426 TACCAGAGAATIGCTCTTAGAACGCCTCCATGATTGAGAGCTGCCTTGGTTCTAGTTATC 357
                                                                                                                                                                                                                                                                                                       366 ATATTCTTGTAGAGTGTGCTGTCCTTTTCCCATTCTTTGATCGCGGTACCTCCAATGGCA 307
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 TIGCATICTIGAGGAAGGAAATGATCCCAAIGAGAACCATGAACTCCTCCCCTGCCCGAC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rice;
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ن
                                 Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rice pyruvate decarboxylase (pdc2) gene promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypoxia inducible promoter; HIP; pyruvate decarboxylase; gene expression; transgenic plant; anti-tumour agent; ss.
                                                              Indels
Sequence 547 BP; 172 A; 116 C; 117 G; 142 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1654 AIGITCGACTGCCCTCCCAGGATGAACACCACCTTGTTCG 1693
                                DB 21;
                              Score 114.4; DB 21;
Pred. No. 1.1e-14;
0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated hypoxia inducible promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP
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AAX32000 standard; DNA; 2380
                                2.3%;
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                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-229236/19
                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hodges TK, Hug E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUN-1999
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                                                           275;
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                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186
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be used for regulating the expression of foreign genes in rice. The HIP can be used for regulating the expression of foreign genes in cells such that the genes are expressed upon exposure of the cells to anaerobic conditions. The HIP can be used to produce transgenic plants that are more tolerant of anaerobic conditions, e.g. ifooding. The HIP can also be used to enhance the expression of gene products that are normally induced under hypoxia conditions. The promoter can be operably linked to genes that express a protein product that is effective against solid tumours pdc2 gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                   4501 GIAGGACCAGGIAITAAGAGTATAGTAAGCAACTATIGTATGAATTAGCTATTACATTAA 4560
                                                                                                                                                                                                                                                                                   4441 ACTATATATTGTAGCCAGCTACAGCACGGACTCAAAGACGTAATGTGTGTATATGACAA 4500
                                                                                                                                                                                                                                                                                                                                                                                                                                  1266 GGTGGACCATATATAATAATATAATAAGCAACTATTGTATGAATGGTTATTCGATTGG 1207
                                                                                                                                                                                                                                                                                                                                                                                   New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar CO39 useful for conferring or improving resistance of plants to strains of Magnaporthe grisea or other plant pathogens with avirulence gene AVRI-CO39
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice, chromosome 11; Indica rice cultivar; CO39; avirulence gene; AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding; resistance; agricultural; horticultural; plant protectant; ds.
                                                                                                                                                                                                               2.2%; Score 107.8; DB 20; Length 5526; 78.1%; Pred. No. 7.3e-13; tive 0; Mismatches 37; Indels 3;
                                                                                                                                                                                   Sequence 5526 BP; 1438 A; 1322 C; 1289 G; 1477 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durfee TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 52-59; 175pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (WISC ) WISCONSIN ALUMNI RES FOUND. (USDA ) US DEPT OF AGRICULTURE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD38801 standard; DNA; 15686 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rice RGA38 contig.26Nippon DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2000; 2000US-242313P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                    Best Local Similarity 78.1 Matches 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-471442/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200234927-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD38801;
                                                                                                                                                                                                                   Query Match
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Job time

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The invention relates to a polynucleotide isolated from chromosome 11 of Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of Magnaporthe grisea having avirulence gene ANEL-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-CO39(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-CO39(t) genes, and to produce large quantities of pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ς,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1 | 1111 | 1 | 111 | 1 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 11 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4301 AATTTTTCAAATAAGACGGATGGTCAAAGCGCTAAACATGGATATCTATGGCTACACTTA 4360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9172 AAATTTTCAAATAAGACAGACGATTAAA--GTTGGGCGCGGAAAACTATGGTTACACTTA 9229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or horticultural applications. The present sequence is rice R6A38 contig. 26Nippon DNA. This sequence comprises portion of BAC clone 82N2O from Nipponbare, containing R6A38 sequence well as obes buss and NBR6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15686 BP; 4645 A; 3184 C; 3204 G; 4653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Searched:

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Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group).

Oryza sativa (japonica cultivar-group)

Bukaryota, Viridiplanitae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Bhrhartoideae; Oryzeae; Oryza.

I (bases 1 to 465)

Sasaki, T. and Yamamoto, K.

Rice CDNA from immature leaf including apical meristem
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Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/

    465
/organism="Oryza sativa (japonica cultivar-group)"

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AZ047724
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Contact: Takuji Sasaki
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                                                                                                            March 25, 2003, 19:50:00 ; Search time 5095.83 Seconds
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15694.084 Million cell updates/sec
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                 GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence:
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EST 02-APR-2002

Tsukuba, Ibaraki

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/organism="Oryza sativa (japonica cultivar-group)"
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BE490225.1 GI:9609758
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzeae; Oryza.
                                          /clone_lib="Rice cDNA from immature leaf including apical
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AU030601 Rice CDNA from immature leaf including apical meristem Oryza sativa (japonica cultivar-group) CDNA clone E51292_22, mRNA
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                         1426 GGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGCGCGTTAGCGAAGGACATC 1485
                                                                                                                                                                                                                                                                                    1486 CCGGGACCGACGCCGCAGGTGCGGTTGCAGTCGATGCCGTTGTGGAGCGGCTCGTGGGCC 1545
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                                                                                     /note="Organ: leaf; immature leaf including apical
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Sasski, r. and ramamoto, k.
Rice cDNA from immature leaf including apical meristem (optilished (1997)
                                                                                                                                                                  DB 9; Length 465;
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Pred. No. 1e-57;
Transfere 5; Indels
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/db_xref="taxon:39947"
                                                                          /dev_stage="immature"
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                            /clone="E51292_1A"
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AU030601.1 GI:3763862
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98.5%;
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Tel: 81-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                             Matches 388; Conservative
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Triticum aestivum Bukaryoch, and indialpantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryoch, Viridialpantae; Streptophyta; Enbryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Tr
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                                      Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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/cultivar="Nipponbare" / /cultivar="Nipponbare" / /cultivar="Nipponbare" / /cultivar="1994"" / /clone="E51200.23 / /cultivar="E51200.23 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 ACAGAGAGGACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGCCAACATATGTC 308
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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/note="Organ: leaf; immature leaf including apical
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Unpublished (2000)
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125 c 118 g 127 t
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Pred. No. 2.9e-50;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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TaE05012F06R TaE05 Triticum aestivum cDNA clone TaE05012F06E, MRNA
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                                                                                                                                                   Contact: Takuji Sasaki
Mational Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Isukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4861
                                                                                                                                                                                                                                                              Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasakieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
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Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe RG, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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Pred. No. 8e-36;
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/note="Green shoot (8 days old)"
94 c 91 g 60 t
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Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 309)
Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
Unpublished (1995)
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            /ultivar="Chinese Spring"

/db_xref="taxon:4565"
/dbone="wherese Spring"
/clone="wherese Spring"
/clone=lip="Where cold-stressed seedling cDNA library"
/tissue_type="Seedling"
/dev_stage="Five-day old seedling"
/lab_host="E. coli SoLR;
/lab_host="E. coli SoLR;
/note="vector: Lambda Uni-ZAP XR, excised phagemid;
/lab_host="E. coli SoLR;
/lab_hos
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                                                                                                                                                                                                                                                                                                                                                                                                           for 48 hr. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give platescript phagemids in the TJ Close lab (Choi. Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1243 GCCATCCGGCGGCGTACTCGTTGGCGTCGCCCAGCGCACGGTGTCGCTCTCCCCCTGG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1363 AGATCGGAGTAGAGGTCGGTGCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1423 CAGGGGACGAGGCCGATGACAG-----GGAACTGGCCGGAGCGAAGGAGGGCGTTAGCG 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1477 AAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGC 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1303 TACCAGAGACAGCGCCGATGCGGCCGCCGGCGTCTCGAGGGCCGACCTGGAGCGGCGGAGG 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1537 ICGIGGGCCICCICCATCGGAGCTGCGGGGAGGGGGGGGGATGGAGGGGTTGGGGGGCG 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AIGTCCGGGRACAGCICCGACCCCITGCCCACTCGGCCATGCCGCGTGCCCCGACGGCG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 ACCTGGATGAGGAGGAGGTGGGGCATGGCGAGGTCCTGCCGGAGGTCGCGGACGACGAGGCG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 CCCATGCGGCGCGCGCGTACTCGCTGGCGTCGGCCCAGCGCTGTCGCTTCTCGCCCTGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 274.2; DB 10
Pred. No. 2.1e-39;
0; Mismatches 78,
organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other authors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA, mRNA sequence.
D47552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D47552.1 GI:701261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 a
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ORIGIN
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KEYWORDS
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plueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon RescueMu tansposon Resigned to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu,' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digsated using BamHI and BglII; and ligated to form circular plasmids. DNIOB cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 22-OCT-2001
                                                                                                                                                         Sequence was trimmed at very probable ligation site. Post-ligation sequence submitted separately. Plate: 1006008 \ row: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF619879 152-OCT-20 HVSWEC0009122f Hordeum vulgare seedling shoot EST library HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGATGACAGGGAAC-----TGGCCGGAGCGAAGGAGGCGTTAGCGAAGGACATCCCG 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1546 TCCTCCCATCGGAGCTGCGGGGAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGG 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1606 GGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCGGGCCCCGGCCATGTTCGACTGC 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1315 GCGCCGATGCGGCCCGCTCTCGAGGCGACCCTGGAGCGGCGGAGGATCGGAGTAG 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1375 AGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCGCAGGGGACGAGG 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 GCACCGATGCGGCCCCCCGTCTCGACGGCGACCCTGGCCGGGCGCACTCTCGGCGTAG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 CCTACCACGGCGCCCCCGCGCGCGCGCGCAGCGCGCGTTGGCGAACGCCATCCCG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1489 GGACCGACGCCGCAGGTGCGGTT - - - GGAGTGCATGCCGTTGTGGAGCGGCTTCTGGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 210.6; DB 17; Length 486; Pred. No. 6.3e-28;
                                                                                                                                                                                                                                                                                                                  /cultivar="mixed background W23/A188/B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Indels
                                                                855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1666 CCICCCAGGAIGAACACCACCITGIICGACGGAGGGAGG 1704
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                       Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                         1. .486
/organism="Zea mays"
                                                                                                                                                                                                                         Class: transposon-tagged.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 9
                                                                                      Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 4.2%;
Best Local Similarity 74.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ampicillin.
                                             Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 296; Conservative
  Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF619879/c
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ORIGIN
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COMMENT
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                                                                                                                                                                                                                                                                                                               /tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="E. coli DHIOB"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI: Site_2: MluL; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"
110 c 115 g 46 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <del>.</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 17-DEC-2001
                   Email: scloutier@em.agr.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb plate: 012 row: F column: 06 Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1566 GGAGAGGCGGAGGATGGAGGGTTGGGGGCGCACTCCGGGGGGAACCATGCCGTCCCAGTG 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1332 GGTCTCGAGGGCGACCCTGGAGCGGCGGACGAGATCGGAGTAGAGGTCGGTGCCCTTGGC 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1452 -----GCCGGAGCGAAGGAGGCCGTTAGCGAAGGACATCCCGGGACCGACGCCGCAGGT 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1272 GGCCCAGCGCACGGTGTCGCTCTCCCCCTGGTACCAGAGACAGCGCCGATGCGGCCGCC 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1392 CCAGTCGGCCATCCTGGTGCCGCCGACGGCGACGGGACGAGGCCGATGACAGGGAACTG 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 GGTCTCCACGGCGCACCCCGGGCGCCCCACCATGTCGTACAGCTCCGACCCCTTGCC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 CGCGCCCCGGGAGCGGAGCACGCGTTGGCGAAAGAATTCCCGGGGCCGACCCCGCACACCCCGCAGGT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 GGCCCAGCGCACGGTGTCGCTCTCGCCCTGGTACCACACCACGCCCCGGTCCGGCCGCC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 GGAGAGGCGGAGGATGGCGCCCGAGGCGCGCAGTCCGGCGCGCCACCCCCGTCCCAGTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ918792 486 bp DNA linear GSS 177
1005008A02.yl 1006 - RescueMu Grid G Zea mays genomic, DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%; Score 230.4; DB 14; Length 78.1%; Pred. No. 1.8e-31; Live 0; Mismatches 76; Indels
                                                                                                                                                                              1. .381
/organism="Triticum aestivum"
/cultivar="Glenlea"
                                                                                                                                                                                                                                               /db_xref="taxon:4565"
/clone="TaE05012F06R"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                          /clone_lib="TaE05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:13388076
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Walbot, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 78.1 Matches 292; Conservative
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hoxb0089H04r CUGI Rice BAC Library Oryza sativa genomic clone nbxb089H04r, DNA sequence.
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1 (bases 1 to 774)
Wing, A.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
1243 GOCATCOGGOGGCGTACTCGTTGGCGTCGGCCCAGGCGCACGGTGTCGCTCTCCCCCTGG 1302
                                                                                                                             1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGCGACG 1362
                                                                                                                                                                                                                                                             1363 AGATCGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                          1423 CAGGGGACGAG-----GCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1474 GCGAAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGC 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 CACGGTACGAGCCCTACCCCGGCGGTGCCTGGGGGCTGCAGCTCCGGGAGAATGGCGGGG 279
                                                              515 TCCACGTTCCCCTGGTATGCCGCCGTTTCGGCATCGGACTATGCATCGCTCTCCCCTGG 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 ATGITGCTCTGCCCTGACAGAAGAAGAAGAAGAAGACGCGCCTGCGGGGAGCAGCGGC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="nbxb0089H04r"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Location/Qualifiers
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Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
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/db_xref="taxon:4530"
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AQ576807.1 GI:4977292
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                                                                                                                                                     Examount vilgate.

Success of the control of control control of control con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Seedling shoot"
/lab_host="TJC121"
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/cultivar="Morex"
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High quality sequence stop: 583.
Location/Qualifiers
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   ivsmcc0009122f, mrna sequence.
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Total hq bases = 342
                                                              BF619879.2 GI:13107874
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Bordeum vulgare.

Hordeum vulgare

Bukaryora, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;

Triticeae; Hordeum.

(Dases 1 to 816)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,

Frisch, D., Arkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons

J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library

Unpublished (2001)
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B1996651
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                                                                                                                                                                                                                                                                                                                                                                                                                158 GAAAAGTAGAACATAAGGTGCGTAGTCTTTAGCTATTTTATCTGATAAAAGAAAAACAAC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 ITTAATTATACCAAGCCAATTCAATAATCATAAGAATGAGTGGTCCATGAAACTAAATAA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 ACAGAGAGCACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGCCAACATATGTC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 ACAGNGNGGNCTAGAGCGNGGAAGTNCCNTAGTTCAAAAAGGNTTGNGCCAACANATGCC 45
                                                                                                                                                                                                                                                                                                                                        Gaps
                                               /organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                      Length 273;
                                                                                                 /db_xrel__com.
/clone="186064"
/clone="186064"
/dev_stage="Priolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
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                                                                                                                                                                                                                                                                                      Score 187.4; DB 9;
Pred. No. 1.1e-23;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
Clemson University Genomics Institute
10 Jordon Dilversity
Tel: 864 656 7288
Fax: 864 656 4293
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Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 372.
Location/Qualifiers
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/db_xref="taxon:4513"
/clone="HVSMEn0004J09f"
                                                                   /cultivar="Nipponbare"
/db_xref="taxon:39947"
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/lab_host="TJC121"
  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             Best Local Similarity 85.3
Matches 191; Conservative
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BI956651/c
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                                                                                                             and subtropies, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mpp (Arumuganatha and Barle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety The 11brary contains 36,864 clones with an average insert size of 2185 Kb providing 10.9 haphoid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.
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AU097543 GI:8860225
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Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magrollophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
                                          HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan 181-298-38-7441
Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4281 ITTTTTTAATATTTTTTTTAATTTTTCAAATAAGACGGATGGTCAAGGGCTAAACATG 4340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4221 TTAGTATTTTTATTAGTGATGATAAAACATGAATAGTACTTTATGTGTGACTAATT 4280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 CCAAAAAAAGCCGTCCTACGCAGTTTTACGTGCTACTACTACCTCCCAAAATAAGTGTA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TIAGTATTITTATTGTTATTATATGATAAAACATAAATAGTACTTTATTGTGACTAA-- 147
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                        /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17; Length 774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 188.4; DB 1
Pred. No. 5.7e-24;
0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4341 GATATCTATGGCTACACTTATTTTGGGACGGAGGTA 4376
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Rice cDNA from etiolated shoot (2000)
Unpublished (2000)
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Similarity 82.6%;
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Best Local Si
Matches 228;
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AU097543/c
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QΫ Q ŏ d δŏ 쉼 a ğ g

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/QD_XXEI=_taxuu:49.7/
/clone_lib="load" = RescueMu Grid I"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="bilload" = RescueMu (engineered from hote="Organ: leaf; Vector: RescueMu (engineered from paluesoript backbone); Site_1: BamHr; Site_2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the site www.zmdb.lastate.edu and follow the links for "RescueMu." Grid I was grown at Barkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were "ransformed and then screened on IB plates with
                                                                                                                         Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008052 row: 18
                                                                                                                                                                                                                                                                                                                 /cultivar="mixed background W23/A188/B73"
                               Stanford University
SS Callifornia Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%; Score 178.6; DB 17; ilarity 74.3%; Pred. No. 3.9e-22; Conservative 0; Mismatches 79;
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              Biological Sciences
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                           /organism="Zea mays"
                                                                                                                                                                                                                     Class: transposon-tagged.
Location/Qualifiers
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BE443619.1
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Matches 255;
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BE443619/c
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Anote="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: ANOI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close was prepared, poly(A) was purified, one primary unamplified cohal library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and equence analysis were set formed at Cugi sequence and analysis were performed at Cugi whore. For more details on library preparation and equence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ. Wing R. Kleinhofs A. Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 257.c 323 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1384 CCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGCGCGCAGGGGACGACGATGACA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1618 TCCCAGTGGGACCCCACCACCACCGCGCCCCGCCATGTTCGACTGCCCTCCCAGGATG 1677
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1008052E03.y1 1008 - Rescuemu Grid I Zea mays genomic, DNA
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Pred. No. 1.9e-22;
0; Mismatches 85; Indels
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Matches 247; Conservative
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ORGANISM
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KEYWORDS
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BE443619 613 bp mRNA linear EST 25-JUL-2000 WHEIL16_B08_D16ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHEIL16_B08_D16, mRNA
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                                                                                                                                            1371 GTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCGCAAGGGGAC 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                    1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1542 GGCCTCCTCCCATCGGAGCTGCGGGAGAGGCGGAGGATGGAGGGGTTGGGGGGTCTC 1601
                                                                                                                                                                                                                                                                                            GAGGCCGATGACAGGGAAC-----TGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGACAT 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1602 CGGGGGAACCATGCCGTCCCAGTGGGACCCCACCACGCCCCCGGCGCCCGGCCATGTTCGA 1661
                                                                                                                                                                                                                389 GTAGAGCTCGGTGCCCCTGCCCCACTCTGCCATCCGCGTGCCTCCCACGGGGGAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1485 CCCGGGACCGACGCCGCAGGTGCGGTT---GGAGTCGATGCCGTTGTGGAGCGGCTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 CGCCTCCTCCAGCGCAGGTCGGGCGAGACGCAGCACCGCGGGGGACGGCGCGCAGTC
                                                                    6
DB 17; Length 394;
                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1662 CIGCCCICCCAGGAIGAACACCACCTIGITCGACGGAGGAGG 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCCCGCCAGGATGAAGACCAGCTTGTTGGACGGCGCACG 47
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/tissue_type="developing seeds"
/dev_stage="5 days after anthesis"
/lab_host="8.coli DH108"
/note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
NotI: Site_2: MluI; mRNA obtained from wheat seeds of
cultivar Glenlea 5 days post-anthesis"

1 100 c 107 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticeae; Triticum.
(bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                 BQ237748 1inear EST 03-MAX-2002 TAE05012F06F TAE05 Triticum aestivum cDNA clone TaE05012F06F, MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wheat functional genomics - Glenlea developing seeds cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 kb Plate: 012 row: F column: 06 Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 CATTGGCATAT ----TTATACCAATCAAATTCATGAATTTTAAAAATGGGGGTGCCAGCG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AAGAGTICAAAGAGGAAATTAACCAGAGTAGAGAGCAAATAAATAATAGGATCCCTTTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 AATIGGAAAATITAATIAIACCAAGCCAATICAATAAATCATAAGAATGAGTGGTCCATGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 GAAAAACAACACAGAGGAGGACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGCC 267
   336 AGCATATGTCCCAGCTGGACCTGAGCCTGGGTGTTAAGATGCAGATGGCCGTCTTGGAAC 277
                                                            328 GCCAAACCCTTTGCATCAACAAATCTCACGTTTCGAAGTTTGATCCCTTTCTGAGCTTCC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                          276 GGCAACCCCATGGCATCGACAAACCTCACGTTCCGAAGTTTTAAGCCCTTCTGAGCTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AAGIGTAACACACTAAIGGTCAICCGIACICAFFGAAIAFGAIGAAGTIGTACIGGGCTA
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195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340
Fax: (204) 983-4604
Email: scloutier@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 446;
                                                                                                                                                                                                            216 CITACGACTICGGTGTACTGCCCAAGCCCTGATGCCAGCCCAACCTGGA 168
                                                                                                                                                                              388 CITACTACTTCAGTATATTGCCCAAGCCCTGATGCTAGTCCTACCTGAA 436
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Pred. No. 4.7e-20;
0; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="TaE05012F06F"
/clone_lib="TaE05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: Dr. Sylvie Cloutier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cultivar="Glenlea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BQ237748.1 GI:20433624
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Local Similarity 66.7%;
les 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                      BQ237748
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//dev_stage="Irio day old etiolated seedling"
//lab_host="E. coli DH10B"
//note="Wector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
instatin and cefotaxime in covered crystalization
dishes: Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Manolliophyta; Lilifopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nquyen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)." 155 c 159 g 145 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Wheat etiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          california, Riverside. The cDNA clones were in vivo exclsed to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguye lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA
                                                                                                                                          Anderson,O.D., Chao,S., Chol,D.W., Close,T.J., Fenton,R.D., Ban,P.S., Esla,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 AATTGGAAAATTTAATTATACCAAGCCAATTCAATAATCATAAGAATGAGTGGTCCATGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 CATTGGCATAT----TTATACCAATCAAATTCATGAATTTTAAGAATGGTGGTGCCAGCG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 AACATATGTCCAAGCTGGACTTGCGCTTGGGTGCTAAGGTGCAGATGGCCATCTTCTAGT 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAACAACACAGAGAGGACTAGAGCGTGGAAGTACCATAGTTCAAATAGGCTTGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="WHE1116_B08_D16"
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California, Riverside.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280; Conservative
   Triticum aestivum
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nbxD0041B05f CUGI Rice BAC Library Oryza sativa genomic clone
nbxb041B05f, DNA sequence.
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Ming.R.A. and Dean.R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998)
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                                                                                                                    4126 TAGAATAGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACG 4185
                                                                                                                                                                                                                                                                                                                                                                                                   4306 TICAAATAAGACGGAIGGICAAAGCGCTAAACAIGGAIATCIAIGGCIACACITAITITG 4365
                                                                                                                                                                                                                                      272 TATACTCCTACTCCTCTGTCCCAAATAAGTGCAGTTTT-GCACTATTCACGTTCAACG 214
                                                                                                                                                                                                                                                                                                                                                                                                                            genome of rice, three times larger than that of
                           DB 17; Length 535;
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/clone_lib="CUGI Rice BAC Library"
                        Score 164.8; DB 17;
Pred. No. 1.1e-19;
0; Mismatches 32;
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Clemson University Genomics Institute
Clemson University
100 Ordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/lab_host="E. coli DH10B"
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Class: BAC ends
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High quality sequence stop: 189.
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/cultivar="Nipponbare"
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                        3.3%;
                                               Best_Local Similarity 85.8
Matches 218; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              AQ573895 53-JUN-1999 abxb0083A09r CUGI Rice BAC Library Oryza sativa genomic clone abxb0083A09r, DNA sequence.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza
                                                                                                                                                                 181 GCT-----ACCAGGAAACTAGTGTTTGAATGTACCATAAGTCAAATAGGACTGAGCC 233
                                                                                         234 AGCATATGTCCCAACTGGACCTGAGCCTGGGTGTTAAAATGCAAATGGCCGTCTTGGAAC 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                               AACATATGTCCAAGCTGGACTTGCGCTTGGGTGCTAAGGTGCAGATGGCCATCTTCTAGT
                                                                                                                                           GGCAAACCCTTTGCATCAACAAATCTCACGTTTCGAAGTTTGATCCCTTTCTGAGCTTCC
                                                                                                                                                                                                                                                             388 CTTACTACTTCAGTATATTGCCCAAGCCCTGATGCTAGTCCTACCTGAA 436
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel. 864 456 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
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/clone="nbxb0083A09r"
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Arabidopsis, makes it suitable for genomic studies. In
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æ 4132 AGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACGTTTGAC 4191 Gaps ı, Query Match 3.3%; Score 163.6; DB 17; Length 842; Best Local Similarity 88.0%; Pred. No. 1.7e-19; Matches 213; Conservative 0; Mismatches 24; Indels 5; BASE COUNT ORIGIN ŏ g

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4312 TAAGACGGATGGTCAAAGCGCTAAACATGGATA--TCTATGGCTACACTTATTTTGGGAC 4369

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/cdCOMB.seq:*
6: /cgn2_6/ptodata/1/ina/cdCOMB.seq:*
             GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-110-390-13

US-09-110-390-13

US-09-110-390-5

US-09-103-840A-2

US-09-103-840A-1

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US-08-105-39

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US-09-105-39

US-09-078-166-1

US-08-97-46-1

US-08-97-46-1

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                US-09-575-574-5/c

Sequence 5, Application US/09575574

Patent No. 6376750

GENERAL INFORMATION:

APPLICANT: Yu, Su-May

APPLICANT: Chao, Yu-Chan

TITLE OF INFORMATION:

FILE REFERENCE: 08919-047001

CURRENT RAPLICANTE: 2000-05-22

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 1730
           US-08-457-342-6
US-08-457-6468-6
US-08-457-6468-6
US-08-457-338-4
US-08-457-3358-6
US-08-214-6
US-09-028-934-6
US-09-029-603-4
US-09-029-603-4
US-09-029-603-4
US-09-029-603-4
US-09-072-596-162
US-09-072-596-162
US-08-343-428-1
US-08-844-1428-1
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US-09-575-574-3/c
; Sequence 3, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
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ORGANISM: Oryza sativa
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US-09-249-585A-4/c
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US-09-130-114-2/c
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Pred. No. 3.6e-12;
0; Mismatches 79; Indels 9
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Pred. No. 8.7e-09;
n: Mismatches 29; Indels
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APPLICANT: YU, SU-MAY
APPLICANT: Chao, Yu-Chan
TITLE OF INVENTION:
GORRERY APPLICANTION UNDERS: US/09/575,574
CURRENT FILING DATE: 2000-05-22
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
ILENGTH: 500
           TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER FILE REPERENCE: 08919-047001
CURRENT APPLICATION NUMBER: US/09/575,574
UUMBER OF SEQ ID NOS: 10
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                                                                                         FastSEQ for Windows Version 4.0
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; Sequence 2, Application US/09575574
; Patent No. 6376750
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Matches 168; Conservative
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Chao, Yu-Chan
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; ORGANISM: Oryza sativa
US-09-575-574-2
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SOFTWARE: FASTS
SEQ ID NO 3
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APPLICANT:
                                                                                                                                       TYPE: DNA
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APPLICANT: HOTIGK, ROBERT
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
PILE REFERENCE: 0867/0D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 18
SEQ ID NO 4
LENGTH: 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Horlick, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 4; Length 1926; Pred. No. 4.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
| LOCATION: (1)..(1926)
| STHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4
Sequence 4, Application US/09249585A Patent No. 6417002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/09130114
; Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.5%;
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Epstein Barr Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 227; Conservative
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4435 CAGCGGACTATATATTTGTAGCCAGCTACAGCACGGACTCAAAGACGTA----ATGTGT 4489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.5%; Score 73.2; DB 4; Length 1026; 75.3%; Pred. No. 5e-08; tive 0; Mismatches 33; Indels 6
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US-09-105-390-5
Sequence 5, Application US/09105390
Sequence 5, Application US/09105390
Parent No. 6288303
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 6
CORRESORDENCE ADDRESS:
ADDRESSEE: Deblinger 6 Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4490 GTATATGACAAGTAGGACCAGGTATTAAGAGTATAGTA 4527
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  SOFTWARE: FastSEQ for Windows Version 2.0 CYREBLY APPLICATION DATA: US/09/105,390 FILING DATE: Filed herewith
                                                                  FILING DATE: Filed herewith
CLASSIFICATION
PRICA APLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-UIN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
FREERRENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
RESISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dehlinger & Associates 350 Cambridge Ave., Suite
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    Diskette
IBM Compatible

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SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 75.3
Matches 119; Conservative
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OPERATING SYSTEM:
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US-09-105-390-13
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COUNTRY:
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                                                                                                                                                                                                                                                                  Length 1931;
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Pred. No. 4.5e-08;
0; Mismatches 255; Indels
TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 0867/1D903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
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Sequence 13, Application US/09105390

Sequence 13, Application US/09105390

PARENT NO. 6288303

TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: Rice Beta-Glucanase Enzymes

TITLE OF INVENTION: and Genes

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dehlinger & Associates

STREET: 350 Cambridge Ave., Suite 250

CITY: Palo Alto

STATE: CA
                                                                                                                                                                                                                                                           1.5%;
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                             ; ORGANISM: EBNA
US-09-130-114-2
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LENGIH: 1931
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                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 CAGCGGGCTACAGATTIGTAACCACCTACAGCAAGACTTTAAGATGCATGTGTATAA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9:
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73.2; DB 4; Length 2169; Pred. No. 7.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Indels
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PPLICATION UMBER: US/08/232,463
PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
102-08-232-463-14/C
15-08-232-463-14/C
15-08-232-14/C
15-08-232-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      1.5%;
                                                                                                                               INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2169 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (703)836-9300
(703)683-4109
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TYPE: nucleic acid
STRANDEDNESS: single
                             : 650-324-0880
650-324-0960
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.5
Best Local Similarity 75.3
Matches 119; Conservative
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                             TELEPHONE:
TELEFAX: 6
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US-09-105-390-5
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STATE:
                                                                                                  TELEX:
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Db 3928207 CGCCGGCCCCCGCCCCGCCGGTGCCCGCCGTCCCCCCGTCGCCGGGAACACCGGCGC 3928148
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                       1382 TGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCAGGGGGACGAGGGCCGATGA 1441
                                                                                                                                                                                                              1241 TGGCCATCCGCCGCGCGTACTCGTTGGCGTCGCCCAGCGCACGGTGTCGCTCTCCCCCT 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRAR APPLICATION NUMBER: US/09/103,840A
CURRAR PELING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                  Gaps
                                                                                                                                                                0
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                                                                                                                 DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 260; Indels
                                                                                                                                                                Indels
                                                                                                              Query Match 1.4%; Score 70.6; DB 1; I Best Local Similarity 5.9%; Pred. No. 6.3e-07; Matches 19; Conservative 194; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1301 GGTACCAGAGGACAGCGCCGA 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, OWEN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 244; Conservative
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; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SEQ ID NO 2
LENGTH: 4403765
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Sequence 4, Application US/09060756

Patent No. 6183957

BEREAL INFORMATION

PAPLICANT: Cole, Stewart

APPLICANT: Gordon, Stewart

APPLICANT: Gordon, Stewart

APPLICANT: Bilault, Alain

ITILE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA

TILLE OF INVENTION: LIBRARA APPLICATION TO THE DETECTION OF WYCOBACTERIA

TILLE REPRENCE: 3495-0169

CURRANT APPLICATION WUMBER: US/09/060,756

CURRANT FILING DATE: 1998-04-16
     DD 1191405 AGCCGGC-CGACCCGCCGTCGCCACCGCGGCCGCCGCCGCCCCCCTCCGCCGCCGCACCG 1191463
                                                                                                    Db 1191285 ceccécerececececececerrececeacade 1191344
                                                                                                                                                                                                         1191345 CGTTGCCGGCGTTGCCGCCGCCGCCGCCGGTGCCGGCGTCGCCGTTGCCGGCACAGCC 1191404
                                                                                                                                                                                                                                                                                                                                                                                               1304 ACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGCGACGA 1363
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                                                      1517 CGATGCCGTTGTGGAGCGGCTCGTGGGCCTCCTCCCATCGGAGCTGCGGGGAGAGCGGGA 1576
                                                                                                                                                           1577 GGATGGAGGGGTTGGGGGGGCGCACTCCGGGGGAACCATGCCGTCCCAGTGGGACCCCACCA 1636
                                                                                                                                                                                                                                                             1637 CGCCCCGCCCCCGCCAFGTTCGACTGCCCTCCCAGGATGAACACCACCTTGTTCGACG 1696
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Pred. No. 6.2e-05;
0; Mismatches 239;
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US-09-060-756-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.2%;
Best Local Similarity 46.0%;
Matches 204; Conservative
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US-09-060-756-4
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Db 3928087 TGCCGCCGTCCCCGCCGATGCCGCCTTGGCCGCCGTCGGGTCGGGTCGGCGATCA 3928028
                                                                                                                                                                                                                                                                                                                                                                                                                                           3927967 FGAFGCCGCCGCCCCCCCCCTFGCCGCCGCCCCCTFGCCCGCTFGGCCGCTFGGCCGCCFTAA 3927908
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                                                                                                                                                                                                                                                                                     1562 GCGGGAAGAGGCGGAAGAGAGGGTTGGG-----GGCGCACTCCGGGGGAACCATGC 1615
                                                                                                                                                                                                                                                                                                                                                                                       1616 CGTCCCAGTGGGACCCCCACCACCCCCCCCCCCCCCCATGTTCGACTGCCCTCCCAGGA 1675
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                                                                                                                                                                                 1502 AGGIGCGGTIGGAGTCGAIGCCGTIGIGGAGCGGCTCGTGGGCCTCCTCCCATCGGAGCT 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRASER, Citaire M.
APPLICANT: FRASER, Citaire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION WUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.
SOFTWARE: Patentin Ver. 2.1
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llarity 46.6%; Pred. No. 0.005;
Conservative 0; Mismatches 287; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 3927728 CCACCGCCGCCCTTTGCCGCCGGTGCCGC 3927698
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CTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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US-09-103-840A-1
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Best Local 3
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CORRESPONDENCE ADDRESS:
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                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-728-956-3
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45.5%; Pred. No. 0.00026;
Live 0; Mismatches 259; Indels 0;
                                                                                                                                                                                                                                                                                                          APPLICANT: Zhao, L. TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hodges, Thomas K.

APPLICANT: McGee, J. D.

TITLE OF INVENTION: Plant Pathogen Induced Proteins
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION UNMBER: US/09/105,537A, CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43 SOFTWARE: RESUSED for Windows Version 3.0 SEQ ID NO 1 LENGTH: 15872
                                                                                                                                                               Sequence 1, Application US/09105537A Patent No. 6265202 GENERAL INFORMATION: APPLICANT: Sherman, D.H. APPLICANT: Liu, H. APPLICANT: Liu, H. APPLICANT: Xue, Y.
              1604 GGGGAACCATGCCGTCGCAGTGG 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-728-956-3
; Sequence 3, Application US/08728956
; Patent No. 5677175
                                          498 GGACACCGGTGGGGACGGCGGGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-1
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                                                                                                                              RESULT 12
US-09-105-537-1/c
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APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Fuerk, Craig
APPLICANT: Filthow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4132 AGTACTCCCTCCGTCTCAAAATAAGTGTAGTTTTAGCACTATTCATGTTCAACGTTTGAC 4191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4252 CATGAATAGTACTTATGTGTGACTAATTTTTTTTTAATATTTTTTATTATTATTTTTTTCAAA 4311
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                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPALIBLE
COMPOTER: IBM PC COMPALIBLE
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 131;
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Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Brean, John P.
REGISTRATION NUMBER: 38,833
RETERRATION NUMBER: 3220-26119
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)231-7745
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1591 base pairs
                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,956
ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09197649 Patent No. 6194550
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Best Local Similarity 54.7
Matches 163; Conservative
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Patent No. 6060234
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
APPLICANT: Stassi, Diane L.
APPLICANT: Stassi, Diane L.
APPLICANT: Ruan, Xiaoan
APPLICANT: Ruan, Xiaoan
APPLICANT: Reada-Lopez, Ana
APPLICANT: Kakayas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
WUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Sequence; other INFORMATION: having a 120 repeat of ACG flanked by fixed; OTHER INFORMATION: fragments having NcoI restriction sites. US-09-197-649-7
                                                                                                                                                                                                                                                                                                                                                                                                 Length 390;
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.2%; Score 60; DB 4; Length 390
Best Local Similarity 48.0%; Pred. No. 4.4e-05;
Matches 171; Conservative 0; Mismatches 185; Indels
CURRENT FILING DATE: 1998-11-23

RARLIER APPLICATION NUMBER: 07/829,461

RARLIER PILING DATE: 1992-01-31

RARLIER APPLICATION NUMBER: 07/739,055

RARLIER PILING DATE: 1991-08-01

RARLIER FILING DATE: 1991-08-02

RARLIER FILING DATE: 1990-08-02

NUMBER OF SEQ ID NOS: 26
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                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIO
OPERATING SYSTEM: DOS
                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Abbott Park
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 60064-3500
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US-08-858-003-1/c
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                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                         SEQ ID NO 7
                                                                                                                                                                                                                                                                           FEATURE:
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1540 TGGGCCTCCTCCCATCGGAGCTGCGGGAGAGGCGGAGGATGGAGGGGTTGGGGGGCGCAC 1599
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Pred. No. 7.2e-05;
0; Mismatches 205;
                                                                  FILING DATE: 16-MMY-1979
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuto
REGISTRATION NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
FILEPRAX: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1500 TCCGGGGAACCATGCCGTCCCAGTGGG 1627
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Job time: 20400.7 secs
SOFTWARE: FastSEQ Version 2.0 CARREDAY APPLICATION DATA.
APPLICATION NUMBER: US/08/858,003 FILING DATE: 16-MAY-1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.2%;
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LENGTH: 925 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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US-08-858-003-1
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March 26, 2003, 05:23:30 ; Search time 275.743 Seconds
   (without alignments)
   15433.627 Million cell updates/sec
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1 aggggacactacactttcca......tgccgccggagtgcgcccg 5001
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574371 seqs, 425486471 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	QI.	Description
	121.8	2.4	!	10	US-09-993-170-56	Sequence 56, Appl
7	118.4	2.4	949	10	US-09-770-445-342	Sequence 342, App
e	114.4	2.3		σ	US-10-101-464A-374	Sequence 374, App
4	111.2	2.2		10	US-09-887-576-870	Sequence 870, App
ς,	83.2	1.7		10	US-09-887-576-859	Sequence 859, App
φ	68.2	1.4		o	US-10-184-644-332	Sequence 332, App
7	61	1.2		10	US-09-974-300-5249	Sequence 5249, Ap
œ	9.09	1.2		σ	US-09-860-846-1	Sequence 1, Appli
σ	60.6	1.2		10	US-09-861-289-1	Sequence 1, Appli
10	9	1.2		10	US-09-790-399-7	Sequence 7, Appli
11	09	1.2	925	თ	US-09-735-056-1	Sequence 1, Appli
12	58	1.2		თ	US-10-125-815-4	Sequence 4, Appli
13	57.4	1.1		12	US-10-032-717-9	Sequence 9, Appli
14	56.4	1.1		10	US-09-878-574-3891	Sequence 3891, Ap
12	55.2	1.1		10	US-09-349-385-11	Sequence 11, Appl
16	54	1.1		10	US-09-969-373-472	Sequence 472, App
17	54	1.7		10	US-09-887-576-832	Sequence 832, App
18	53.2	1.1		σ	US-09-860-846-34	Sequence 34, Appl
13	53.2	1.1		10	US-09-861-289-34	Sequence 34, Appl

RESULT 2 US-09-770-445-342

Sequence 30, Appl Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 32, Appl Sequence 32, Appl Sequence 32, Appli Sequence 32, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 39, Appl Sequence 39, Appli Sequence 36, Appl Sequence 36, Appl Sequence 36, Appli Sequence 804, Appli Sequence 804, Appli Sequence 805, Appli Sequence 206, Appli Sequence 206, Appli Sequence 206, Appli Sequence 206, Appli Sequence 206, Appli	esistance Gene	; DB 10; Length 5757; .1e-20; es 22; Indels 2; Gaps 1; TAGCAGGGACTATATATTGTAGC 4456
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13842 9 36778 9 36778 9 9 36778 10 2294 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 2712 10 271	US/0 A1 A1 A1 Cory Cory Cory NB WB NB WB NB NB NB NB NB NB NB NB NB N	2.4%; y 86.0%; rvative AAGAGATAAA
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01000000000000000000000000000000000000	SULT 1 -09-993 Sequence Sequence Settler N APPLICAL APPLICAL TITLE OI TITLE OI FILE REI CURRENT CURRENT PRIOR F ROUMENT PRIOR F SOFTWAR SEQ ID N TYPE: I TYPE: I	Query Ma Best Loc Matches 4397 3259 4457 3319 3377
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SERRICAL THEORAGHICON:

APPLICANT: NIEUWenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Highins, Colleen M.
TITLE CF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: 09/704,302
FRIOR APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/728,986
PRIOR PRILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-11-01
PRIOR FILING DATE: 1909-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTCTCCCCCTGG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1303 TACCAGAGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCCTGGAGCGGCGGAGC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1363 AGATCGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGA-----AGGAGGGCGTTA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1474 GCGAAGGACATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGC 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1534 GGCTCGTGGGCCTCCTCCCATCGGAGCTGCGGGAGAGAGGCGGAGGATGGAGGGTTGGGG 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1594 GOGCACTCCGGGGGAACCATGCCGTCCCAGTGGGACCCCACGCCCCCCGCGCCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426 TACCAGAGAATTGCTCTTAGAACGCCTCCATGATTGAGAGCTGCCTTGGTTCTAGTTATC 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 APATTCTIGTAGAGTGTGCTGTCCTTTTCCTTTGATCGCGGTACCTCCAATGGCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 ACCIGGAIGAAAAGGAGAICGGGAIGITICAGAICAGAGCGGAIAICAIGGAIAAGICIC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 ICGAGATTATGTTTATAGCTATTAGCATTCTTCTCAGATTCTGTATCACTTTCGCCTTGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 IIGCAIICTIGAGGAAGGAAIGAICCCAAIGAGAACCAIGAACICCICCCCCGGCGGC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 547;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 114.4; DB 9;
Pred. No. 4.2e-19;
0; Mismatches 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AIGITGCTCTGTCCTGAGAACGAAGATATCCATITTCG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 989
SOFTWARE FEATSEQ for Windows Version 4.0
SEQ ID NO 374
LENGTH: 547
                                                                      Sequence 374, Application US/10101464A Publication No. US20030046728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.3%;
Best Local Similarity 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pinus radiata
                                                   JS-10-101-464A-374/C
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US-09-887-576-870/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pinu
US-10-101-464A-374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGTGGGCCTCCTCCCATCGGAGCTGCGGGGAGAGGCGGAGGATGGAGGGGTTGGGGGCC 1596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 TACCACAACACCGCCTTGATCTCTCGCCGCATTTCCTACTCTCCTCCTTCTTGACC 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460 TCCATATTGTTCCCGTAGCTCTCGGCGTCATGGATGTCCAACACGTCACTCTCTTCTTGA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 ATCCTCGTACAAGTGGCTTCCACGCTCCACTCTTTATCGCCGTTCCACGGAAGCG 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed Sequences of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: thaliana
FILE REFERENCE: 2023US (PARA-012PRV)
CURRENT APPLICATION NUMBER: US/09/770,445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
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Sequence 342, Application US/09770445
                                                                                                                                                                                                                                              Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
Garcia, Carlos A.
Kricker, Maja
Slader, Ted
                                                                                             An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                               Yu, Yang
Rameaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis, Keith R.
Allen, Keith
Hoffman, Neil
Hurban, Patrick
                         US20020023281A1
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 342
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APPLICANT:
                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TWVRVSHEHILLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAK 180
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                                                                                                                       Length 2000;
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 332
                                                                                                                       Score 83.2; DB 10;
Pred. No. 1.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68.2; DB 9;
Pred. No. 3.2e-07;
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                                                                                                                                                           0; Mismatches
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Publication No. US20030044930A1
GENERAL INFORMATION:
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20.18;
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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1.4%
Best Local Similarity 20.1%
Matches 88; Conservative
                                                                                                                     Query Match
Best Local Similarity 69.65
Matches 128; Conservative
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Smith, Victoria
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                                      ; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-887-576-859
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) ORGANISM: Homo Sapien
US-10-184-644-332
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US-10-184-644-332
                          LENGTH: 2000
      SEQ ID NO 859
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                                                                                                            APPLICANT: Zhu, T.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Gang, X.
APPLICANT: Cooper, Sret
TITLE OF INVENTION: Promoters for regulation of plant expression
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APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
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Pred. No. 7.4e-18;
0; Mismatches 33;
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CURRENT APPLICATION NUMBER: US/99/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-33
PRIOR FILING DATE: 2000-06-33
PRIOR FILING DATE: 2000-06-23
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SED ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/887,576 CURRENT FILING DATE: 2001-06-25
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Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: BIGMOUTH, P.
APPLICANT: Brown, D.
Sequence 870, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION:
APPLICANT: Budworth, P.
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Best Local Similarity 81.4%;
Matches 166; Conservative
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US-09-887-576-870
                                                                              Brown, D.
Chang, H.
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Best Local Similarity
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LENGIH: 2000
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APPLICANT:
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US/09860846
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Best Local Similarity 45.5%;
Matches 216; Conservative
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Patent No. US20020164742A1
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Best Local Similarity
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US-09-860-846-1/c
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241 GETGTKGEKGDIGLPGSKGDRGWKGDAGVWGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQ 300
                                                                                                                                                             301 GQPGLQGVPGPPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGSPGGRAGLPGSPGSPGATGLKGSKGDTGLQGQQ 360
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Patent No. US2000146721A1
GENERAL INFORMATION:
APPLICANT: BerKa, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085-500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO 5249
LENGTH: 863
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US-09-974-300-5249
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1387 TTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCGCAGGGGACGAGGCCGATGACAGGG 1446
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1565 GGGAGAGGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGGGGGAACCATGCCGTCCCAGT 1624
                                       5178 AGGGACTCGACCTCGGCCTCGCCCGCCTGCACGGCGATCATCGCGCCCCCTCGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DAN encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 0.00039;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/860,846
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
NUMBER OS SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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STREET: 100 Abbott
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
                                                                                                                                                                                                                                                                    OTHER INFORMATION:
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US-09-735-056-1/c
                                                                                                                                                                                     LENGTH: 390
                                                                                                                                                                                                                                                                                                                             US-09-790-399-7
                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                         OTHER
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APPLICANT: Tuerk, Craig
APPLICANT: Fribnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEXO2/C1-CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5058 ACACCGGCGACGTGCGCGGCGGCGACGACGGAGTGGCCGGTGAGCAGGTCGGGG 4999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                       TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/861,289
CURRENT FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: 09/105,537
PRIOR FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60.6; DB 10;
Pred. No. 0.00039;
0; Mismatches 259;
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 15872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/790,399
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/197,649
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA CRGANISM: Streptomyces venezuelae US-09-861-289-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09790399
Patent No. US20020038000A1
GENERAL INFORMATION:
Sequence 1, Application US/09861289 Patent No. US20020110897A1
                                                                                                                                                                                                                                                                                                                                                                                                                            1.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 45.5 Matches 216; Conservative
                                      GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-790-399-7
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCAGCGCACGGTGTCGCTCTCCCCCTGG 1302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGAC 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1483 ATCCCGGGACCGACGCCGCAGGTGCGGTTGGAGTCGATGCCGTTGTGGAGCGGCTC 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1303 TACCAGAGGACAGCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCTTGGAGCGGCGGCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: Description of Artificial Sequence: Sequence INFORMATION: having a 120 repeat of ACG flanked by fixed INFORMATION: fragments having NcoI restriction sites.
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APPLICANT: Atasi, Diane L.
APPLICANT: Summers Dr., Richard G.
APPLICANT: Runners Dr., Richard G.
APPLICANT: Rano, Xiaoan
APPLICANT: Rekavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.2%; Score 60; DB 10; Length 39 Best Local Similarity 48.0%; Pred. No. 3.3e-05; Matches 171; Conservative 0; Mismatches 185; Indels
PRIOR FILING DATE: 1998-11-23
PRIOR APPLICATION WUMBER: 07/829,461
PRIOR PILLING DATE: 1992-01-31
PRIOR APPLICATION NUMBER: 07/739,055
PRIOR PILLING DATE: 1991-08-01
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR APPLICATION NUMBER: 07/561,968
PRIOR PILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Rd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09735056
Publication No. US20030013662A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-10-032-717-9/c
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APPLICANT: Hu, Zhihao

APPLICANT: Hu, Zhihao

APPLICANT: Santi, Daniel V.

TITLE OF INVENTION: RECOMBINANT POLYKETIDE SYNTHASE GENES

FILE REPREBRUCE: 300622004720

CURRENT APPLICATION NUMERS: US/10/125,815

CURRENT APPLICATION NUMERS: US/679,279

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMERS: 60/190,024

PRIOR FILING DATE: 2000-10-04
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Pred. No. 6.4e-05;
                                                                                                                                                                                                                                                                                                                                                  NAME: Dianne Casuto
REGISTRATION NUMBER: P-40,943
REPERBENCE/POCKET WINBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847)-938-3137
TELEPHONE: (847)-938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1600 TCCGGGGGAACCATGCCGTCCCAGTGGG 1627
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                                                                               US/09/735,056
                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/858,003
FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10125815 Patent No. US20020173008A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.2%;
Best Local Similarity 47.2%;
Matches 183; Conservative
                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: uncleic acid
STRANDEDRESS: double
                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-09-735-056-1
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GENERAL INFORMATION:

APPLICANT: Addre R. Aad

APPLICANT: Addre R. Aad

APPLICANT: Micholas B. Duck

APPLICANT: Micholas B. Duck

APPLICANT: Micholas B. Duck

APPLICANT: Theodore W. Kahn

APPLICANT: Lynn E. Sins

TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

TITLE OF INVENTION: Pesticidal Activity Against Coleopterans

FILE REFERENCE: 35718/237005

CURRENT FILING DATE: 2001-10-23

PRIOR FILING DATE: 200-10-24

NUMBER OF SEQ ID NOS: 48

SOFINE OF SECENTION UNINGER VERSION 4.0

SEQ ID NO 9

FENNING: ASSESSION OF SECENTION OF SECENTIANT 
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Pred. No. 0.00015;
0; Mismatches 175; Indels
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CHER INFORMATION: Maize optimized Cry1218-1
NAME/KEY: misc_feature
LOCATION: (0)...(0)
COTHER INFORMATION: mol218-1
US-10-032-717-9
PRIOR APPLICATION NUMBER: 60/158,305
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASESQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 615
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Best Local Similarity 48.2%;
Matches 163; Conservative (
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ORGANISM: Artificial Sequence
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1069 GAGGAIGGCGACCAIGIGGTCGTCGTCGCCTCGTCACCCICGAGGGAGAGGAGCAC 1010
1303 TACCAGAGGACAGCGCCGATGCGGCCGGTCTCGAGGGCGACCCTGGAGCGCGGCGGACG 1362
                                                                                       1363 AGATOGGAGTAGAGGTCGGTGCCCTTGGCCCAGTCGGCCATCCTGGTGCCGCCGACGGCG 1422
                                                                                                                                                                                     1423 CAGGGGACGAGGCCGATGACAGGGAACTGGCCGGAGCGAAGGAGGGCGTTAGCGAAGGAC 1482
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                           889 GACGTIGCTIGGGICGTACAGGICGGCGAGCCAGGGGAGGTGGICGGACCAGTIGAAGGC 830
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Patent No. US20020122492A1
GENERAL INFORMATION:
APPLICANT: Ito, Toshiro
APPLICANT: Fromm, Michael
APPLICANT: Meyerowitz, Elliot
TITLE OF INVENTION: PLANTS HAVING SEEDLESS FRUIT
FILE REFERENCE: MBI-0002
CURRENT FILING DATE: 1999-07-09
FRALIER APPLICATION NUMBER: 0S/09/349,385
CURRENT FILING DATE: 1999-01-15
FRALIER APPLICATION NUMBER: 60/115,967
FRALIER APPLICATION NUMBER: 60/115,967
FRALIER PILING DATE: 1999-01-15
SOFTWARE: Patentin Ver: 2.0
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Pred. No. 0.002;
0; Mismatches 258;
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ilarity 44.9%;
Conservative
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Best Local Similarity
Matches 210; Conserva
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US-09-349-385-11/c
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APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REPERBACE: 38-21(15401)B
CURRENT APPLICATION NUMBER: 05/09/878,574
CURRENT APPLICATION NUMBER: 05/333,535
PRIOR PLILING DATE: 2001-12-21
PRIOR FILING DATE: 1999-06-14
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                                                                                                        563
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                                                                Gaps
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                 Length 2010;
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            Score 57.4; DB 12; Length
Pred. No. 0.00054;
0; Mismatches 286; Indels
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ORGANICAN. Glycine max

OTHER INFORMATION: Clone ID: LIB3028-004-Q1-B1-E11
US-09-879-574-3891
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              1.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 47.5%;
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SEQ ID NO 3891
LENGTH: 405
                                                           Matches 229; Conservative
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                                Similarity
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US-09-878-574-3891/c
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              Query Match
                                          Local
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Total number of pages: 11

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